

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

STAFF USE ONLY

Searcher: Q. Veen - Jaly

Searcher Phone #: 308-4501

Searcher Location: Biotec Lib.

Date Searcher Picked Up: 7/3/01

Date Completed: 7/3/01

Searcher Prep & Review Time: _____

Clerical Prep Time: 3 mi

Online Time: 2 mi

Type of Search

NA Sequence (#) _____

AA Sequence (#) 1

Structure (#) _____

Bibliographic _____

Litigation _____

Fulltext _____

Patent Family _____

Other _____

Vendors and cost where applicable

STN _____

Dialog _____

Questel/Orbit _____

Dr. Link _____

Lexis/Nexis _____

Sequence Systems ABSS02

WWW/Internet _____

Other (specify) _____

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2001, 16:13:43 ; Search time 23 Seconds

(without alignments)
1241.474 Million cell updates/sec

Title: US-09-454-223-2

Perfect score: 2487
Sequence: 1 MLPFLMLVLLVPLGNLGA.....TDPQGVSHGTGFTSGILKL 471

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 412676
Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq_0601:*

- 1: /SIDSB/gcgdata/geneseq/geneseq/AA1980.DAT:*
- 2: /SIDSB/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /SIDSB/gcgdata/geneseq/geneseq/AA1982.DAT:*
- 4: /SIDSB/gcgdata/geneseq/geneseq/AA1983.DAT:*
- 5: /SIDSB/gcgdata/geneseq/geneseq/AA1984.DAT:*
- 6: /SIDSB/gcgdata/geneseq/geneseq/AA1985.DAT:*
- 7: /SIDSB/gcgdata/geneseq/geneseq/AA1986.DAT:*
- 8: /SIDSB/gcgdata/geneseq/geneseq/AA1987.DAT:*
- 9: /SIDSB/gcgdata/geneseq/geneseq/AA1988.DAT:*
- 10: /SIDSB/gcgdata/geneseq/geneseq/AA1989.DAT:*
- 11: /SIDSB/gcgdata/geneseq/geneseq/AA1990.DAT:*
- 12: /SIDSB/gcgdata/geneseq/geneseq/AA1991.DAT:*
- 13: /SIDSB/gcgdata/geneseq/geneseq/AA1992.DAT:*
- 14: /SIDSB/gcgdata/geneseq/geneseq/AA1993.DAT:*
- 15: /SIDSB/gcgdata/geneseq/geneseq/AA1994.DAT:*
- 16: /SIDSB/gcgdata/geneseq/geneseq/AA1995.DAT:*
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- 18: /SIDSB/gcgdata/geneseq/geneseq/AA1997.DAT:*
- 19: /SIDSB/gcgdata/geneseq/geneseq/AA1998.DAT:*
- 20: /SIDSB/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /SIDSB/gcgdata/geneseq/geneseq/AA2000.DAT:*
- 22: /SIDSB/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1110	44.6	261	14	AA36701
2	1110	44.6	261	15	AA53969
3	1110	44.6	261	15	AA57469
4	1110	44.6	261	16	AA85486
5	1110	44.6	261	18	AA34659
6	1110	44.6	261	19	AA71751
7	1110	44.6	261	19	AA41178
8	1110	44.6	261	20	AA39938
9	1110	44.6	261	20	AA25155
10	1110	44.6	261	21	AA96993
11	1110	44.6	261	22	AA67612

12	1110	44.6	261	22	AA37806
13	1110	44.6	294	18	AA09122
14	1105	44.4	294	18	AA09119
15	1104	44.4	294	18	AA09121
16	1102	44.3	226	15	AA49548
17	1101	44.3	294	18	AA09120
18	1100	44.2	261	18	AA09114
19	1099	44.2	261	16	AA76125
20	1099	44.2	261	18	AA09113
21	1099	44.2	294	18	AA09129
22	1098	44.1	261	18	AA09115
23	1098	44.1	261	18	AA09116
24	1094.5	44.0	273	20	AA09118
25	1094.5	44.0	273	20	AA39940
26	1089	43.8	473	14	AA36703
27	1089	43.8	473	20	AA39939
28	1086	43.7	294	18	AA09123
29	1064	42.8	375	21	AA77990
30	939.5	37.8	260	21	AA58217
31	921.5	37.1	211	21	AA58218
32	907.5	36.5	260	21	AA58215
33	889.5	35.8	211	21	AA58216
34	879	35.3	371	16	AA75642
35	831	33.4	260	19	AA753970
36	831	33.4	260	19	AA41179
37	831	33.4	260	20	AA39937
38	829.5	33.4	351	18	AA18780
39	829.5	33.4	351	18	AA13672
40	827	33.3	260	19	AA71750
41	825	33.2	260	14	AA36702
42	812	32.6	280	20	AA39941
43	807	32.4	177	18	AA10874
44	805	32.4	177	18	AA10873
45	769	30.9	182	18	AA09126

ALIGNMENTS

RESULT 1	AA36701	standard; Protein; 261 AA.
XX	AA36701;	
AC	12-AUG-1993	(first entry)
XX	CD40-L.	
XX	Human: CD40-L; CD40; type II; membrane; polypeptide; extracellular;	
KW	transmembrane; region; intracellular; soluble; activity; B cell;	
KW	proliferation; induction; antibody; secretion; Igs; agonist;	
KW	antagonist; binding assay.	
XX	Homo sapiens.	
OS		
FT	Key	Location/Qualifiers
FT	Region	47..261
FT		/note="Extracellular region"
PN	W09308207-A.	
PD	29-APR-1993.	
XX	23-OCT-1992;	92WO-US08990.
PF	25-OCT-1991;	91US-0783707.
PR	05-DEC-1991;	91US-0805723.
XX	(IMMUNEX CORP.	
PA	Armlage RJ, Fanslow WC, Spriggs MK;	
XX		
PI		
XX		

DR WPI: 1993-152417/18.
DR N-PSDB: AAO41506.

PT New cytokine CD40-L as CD40 agonist and antagonist - is used for
PT treating allergies, lupus, rheumatoid arthritis,
PT graft-versus-host disease and insulin-dependent diabetes mellitus
PS Claim 1: Fig 2: 80pp; English.

CC This sequence represents human CD40-L polypeptide which binds to CD40.
CC CD40-L is a type II membrane polypeptide which has an extracellular
CC region at its C-terminus, a transmembrane region and an
CC intracellular region at its N-terminus. A soluble form of CD40-L
CC lacks the transmembrane domain. CD40-L activity is mediated by
CC binding with CD40 and induces B cell proliferation and induction of
CC antibody secretion, including IgE. Membrane bound CD40-L acts as a
CC CD40 agonist and soluble CD40-L acts as a CD40 antagonist. CD40-L
CC can be used in a binding assay to detect cells expressing CD40.

XX Sequence 261 AA;

Query Match 44.6%; Score 1110; DB 14; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.3e-73;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 HRLDKIEDERNHEDVFEMKTTORCTGERSLSLNCSEIKSQEFGVMDMLNKEETK 316
DB 47 HRLDKIEDERNHEDVFEMKTTORCTGERSLSLNCSEIKSQEFGVMDMLNKEETK 106
QY 317 KENSFEMQKQDNPQIAAHYISEASSKTTSVLOWAEKGYTMSNNLYLLENGKQLTVKRQ 376
DB 107 KENSFEMQKQDNPQIAAHYISEASSKTTSVLOWAEKGYTMSNNLYLLENGKQLTVKRQ 166
QY 377 GLYXYTAOYTFCSNREASSAPFIASLCLKSPGRFERILLRAANTHSSAKPCGOOSIHG 436
DB 167 GLYXYTAOYTFCSNREASSAPFIASLCLKSPGRFERILLRAANTHSSAKPCGOOSIHG 226
QY 437 GVFELOPGASVFNVTDPQSVSHGTGTSGLLKL 471
DB 227 GVFELOPGASVFNVTDPQSVSHGTGTSGLLKL 261

RESULT 2
ID AAR53969 standard; Protein: 261 AA.
AC AAR53969;

DT 11-JAN-1995 (first entry)

XX Human CD40-L type II transmembrane protein.

KW Leucine zipper; trimerisation; trimeric CD40-L; fusion protein;
KW hetero-oligomer; homo-oligomer; type II transmembrane protein;
KW soluble CD40-L; tumour necrosis factor family.

OS Homo sapiens.

XX Key Location/Qualifiers
XX Region 50..261

XX /label= extracellular_region
XX /note= "soluble CD40-L"

PN MO9410308-A.

PD 11-MAY-1994.

PF 20-OCT-1993; 93WO-US10034.

PR 23-OCT-1992; 92US-0969703.
PR 13-AUG-1993; 93US-0107353.
XX

PA (IMMV) IMMUNEX CORP.

PI Springs MK, Srinivasan S;

DR WPI: 1994-167465/20.

DR N-PSDB: AAR53969.

PT Prepn. of soluble oligomeric mammalian proteins - using host
PT cells to express a fusion protein comprising a leucine zipper
PT domain and a heterologous mammalian protein

PS Example 1: Page 24; 35pp; English.

CC A DNA fragment encoding the extracellular (soluble) region of human
CC CD40-L was ligated to a synthetic oligonucleotide sequence coding
CC for a leader peptide, a 33 amino acid leucine zipper sequence
CC (AAR53968) and the flag (RPM) linker sequence. Cells expressing the
CC fusion construct are grown to accumulate oligomeric, soluble CD40-L
CC in the supernatant. The leucine zipper sequence spontaneously
CC trimerises in solution and fusion proteins comprising
CC the sequence fused to a heterologous mammalian protein also form
CC oligomers.

XX Sequence 261 AA;

Query Match 44.6%; Score 1110; DB 15; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.3e-73;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 HRLDKIEDERNHEDVFEMKTTORCTGERSLSLNCSEIKSQEFGVMDMLNKEETK 316
DB 47 HRLDKIEDERNHEDVFEMKTTORCTGERSLSLNCSEIKSQEFGVMDMLNKEETK 106
QY 317 KENSFEMQKQDNPQIAAHYISEASSKTTSVLOWAEKGYTMSNNLYLLENGKQLTVKRQ 376
DB 107 KENSFEMQKQDNPQIAAHYISEASSKTTSVLOWAEKGYTMSNNLYLLENGKQLTVKRQ 166
QY 377 GLYXYTAOYTFCSNREASSAPFIASLCLKSPGRFERILLRAANTHSSAKPCGOOSIHG 436
DB 167 GLYXYTAOYTFCSNREASSAPFIASLCLKSPGRFERILLRAANTHSSAKPCGOOSIHG 226
QY 437 GVFELOPGASVFNVTDPQSVSHGTGTSGLLKL 471
DB 227 GVFELOPGASVFNVTDPQSVSHGTGTSGLLKL 261

RESULT 3
ID AAR57469 standard; Protein: 261 AA.
AC AAR57469;

DT 23-MAR-1995 (first entry)

XX CD40 ligand.

KW Probe; primer; PCR; amplify; polymerase chain reaction; detection;
KW mutation; CD40 ligand gene; IGM; ss.

XX Synthetic.

PN MO9417196-A.

PD 04-AUG-1994.

PF 21-JAN-1994; 94WO-US00786.

PR 22-JAN-1993; 93US-0009258.
PR 20-JAN-1994; 94US-0184422.
XX

PA (IMMV) IMMUNEX CORP.

PI Armitage RJ, Davison BL, Fanslow WC, Renshaw BR;
 PI Spriggs MK, Wildner MB;
 DR WPI: 1994-264109/32.
 DR N-PSDB: AAO67123.
 XX
 PT Method for detecting mutation in CD 40 ligand gene - comprises
 PT amplification of nucleic acid, and mutational analysis
 XX
 PS Disclosure; Page 22-24; 38pp; English.
 XX
 CC This sequence is encoded by the CD40 ligand gene. Mutations within
 CC the CD40 ligand gene were identified by the method of the invention.
 CC The method comprises isolating DNA from an individual and selectively
 CC amplifying the isolated DNA derived from the CD40 ligand gene. The
 CC amplification product is then analysed to determine if there is a
 CC mutation present and determining if a protein expressed from the
 CC ligand gene will bind CD40. The detection of mutations in the CD40
 CC ligand gene allows subsequent treatment of a syndrome resulting in
 CC elevated levels of serum IgM and diminished levels of other Ig
 CC isotypes, due to mutation in the CD40 ligand gene. I.e. X-linked
 CC hyper-IgM syndrome.
 CC
 CC Sequence 261 AA;
 SQ
 Query Match 44.6%; Score 1110; DB 15; Length 261;
 Best Local Similarity 100.0%; Pred. No. 1.3e-73;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 OY 257 HRLDKIEDERLHEDFVFMKTTQRCNTGERSLSLNCCEIKSQEGVVKDMLNKEETK 316
 DB 47 hrldkiedernhedfvmkttrcngtgerslsllnceelksqegfvkdmlnkeetk 106
 OY 317 KENSEFMKGDDNPQIAAHVISEASSKTTSVLQWAEKGYTMSNNLVLENKQLTVRKQ 376
 DB 107 kensfemkgddnpqiaahviseasskttsvlqwaekgytmsnnlvlenkgqltvkrq 166
 OY 377 GLYIYAQVTFCSNREASSQAPFIASLCLKSPGRFERILLAAANTHSSAKPCGQGSIHG 436
 DB 167 glylyiaqvtfcsnreassqapfiaslclksprferillraanthssakpcgqgsihg 226
 OY 437 GVFEIQPGASVFVNVTDPQSQVSHGTGFTSFGLLKL 471
 DB 227 gvfeiqpgasvfvnvt dpqsqvshgtgftsfgllkl 261
 XX
 RESULT 4
 AAR85486
 ID AAR85486 standard; Protein: 261 AA.
 XX
 AC AAR85486;
 XX
 DT 18-MAR-1996 (first entry)
 XX
 DE Human CD40 ligand.
 XX
 KW High density membrane-bound CD40 ligand; B-lymphocyte; B-cell;
 KW differentiation; proliferation; baculovirus; Spodoptera frugiperda;
 KW Sf9; insect cell culture; tumour necrosis factor receptor.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT Modified-site 6..8
 FT Domain /label= N-glycosylation_site
 FT 23..46
 FT /label= Transmembrane_domain
 FT Modified-site 239..241
 FT /label= N-glycosylation_site
 XX
 PN MO9529935-A1.
 XX

PD 09-NOV-1995.
 XX
 XX 28-APR-1995; 95WO-US05448.
 XX
 XX 28-APR-1994; 94US-0234580.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.
 XX
 PI Castle BE, Kehry M;
 XX
 DR WPI: 1995-393038/50.
 DR N-PSDB: AAT05763.
 XX
 PT High density membrane bound CD40 ligand - for stimulating the
 PT proliferation of B cells in vitro or in vivo, partic. for producing
 PT differentiated cells
 XX
 PS Disclosure; Fig 1; 74pp; English.
 XX
 CC Human high-density, membrane-bound (hdmB) CD40 ligand (AAR85486) is a
 CC type 2 membrane glycoprotein expressed in activated T-cells. It is
 CC a member of the tumour necrosis factor receptor family. hdmB-CD40
 CC induces long-term proliferation of B-cells in culture. These
 CC proliferating B-cells can be induced to differentiate into antibody-
 CC prodg. cells. Proliferation and differentiation in the presence of an
 CC antigen preferentially proliferates or selects differentiating B-cells
 CC to produce antibodies specific to that antigen. Recombinant hdmB-CD40
 CC is obtd. by incorporating encoding DNA (AAT05763) into a baculovirus
 CC vector that is then used to transfect Sf9 insect cells.
 CC
 CC Sequence 261 AA;
 SQ
 Query Match 44.6%; Score 1110; DB 16; Length 261;
 Best Local Similarity 100.0%; Pred. No. 1.3e-73;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 OY 257 HRLDKIEDERLHEDFVFMKTTQRCNTGERSLSLNCCEIKSQEGVVKDMLNKEETK 316
 DB 47 hrldkiedernhedfvmkttrcngtgerslsllnceelksqegfvkdmlnkeetk 106
 OY 317 KENSEFMKGDDNPQIAAHVISEASSKTTSVLQWAEKGYTMSNNLVLENKQLTVRKQ 376
 DB 107 kensfemkgddnpqiaahviseasskttsvlqwaekgytmsnnlvlenkgqltvkrq 166
 OY 377 GLYIYAQVTFCSNREASSQAPFIASLCLKSPGRFERILLAAANTHSSAKPCGQGSIHG 436
 DB 167 glylyiaqvtfcsnreassqapfiaslclksprferillraanthssakpcgqgsihg 226
 OY 437 GVFEIQPGASVFVNVTDPQSQVSHGTGFTSFGLLKL 471
 DB 227 gvfeiqpgasvfvnvt dpqsqvshgtgftsfgllkl 261
 XX
 RESULT 5
 AAW34669
 ID AAW34669 standard; Protein: 261 AA.
 XX
 AC AAW34669;
 XX
 DT 16-FEB-1998 (first entry)
 XX
 DE Amino acid sequence for CD40L, a novel cytokine ligand for CD40.
 XX
 KW Cytokine; activated CD4+ T cell; CD40; CD40L; monoclonal antibody;
 KW neoplastic cell proliferation; B-cell lymphoma; immune deficiency; AIDS;
 KW melanoma; carcinoma.
 XX
 OS Homo sapiens.
 XX
 PN US5674492-A.
 XX
 PD 07-OCT-1997.
 XX

XX 21-DEC-1994; 94US-0360923.
 PF 23-DEC-1993; 93US-0172664.
 XX (IMMUNEX CORP.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Armitage RJ, Fanslow WC, Longo DL, Murphy WJ;
 DR WPI: 1997-502273/46.
 DR N-PSDB; AAV93782.
 XX
 PT Treating or preventing neoplastic disease associated with
 PT CD40-expressing cells - particularly B-cell lymphoma, by
 PT administration of CD40-binding protein, preferably antibody or
 PT soluble CD40-ligand
 XX
 PS Disclosure: Columns 21-24; 21pp; English.
 CC
 CC The present sequence represents the amino acid sequence of a novel
 CC cytokine ligand for CD40 called CD40L. CD40L is a type II membrane
 CC polypeptide, which is expressed by activated CD4+ T cells. It has an
 CC extracellular region at its C-terminus, and an intracellular region at
 CC its N-terminus. The protein can be used to produce monoclonal antibodies,
 CC which in turn bind to CD40-expressing cells. This inhibits binding of
 CC soluble CD40 to its ligand CD40L. The monoclonal antibody against CD40L
 CC is used to inhibit proliferation of neoplastic cells, and is particularly
 CC useful in treating B-cell lymphoma (e.g. where induced after transplants
 CC or in other cases of immune deficiency such as AIDS), and also melanoma
 CC or carcinoma. Since the monoclonal antibodies inhibit neoplastic cells
 CC directly, they may not need to be coupled to a toxin or radioisotope,
 CC avoiding toxic effects on normal B cells.
 CC
 SQ Sequence 261 AA:
 44.6%; Score 1110; DB 18; Length 261;
 Best Local Similarity 100.0%; Pred. No. 1.3e-73;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 257 HRLDKIEDERNLHEDFVFMKTQRCNTGERSLSLNCETIKSFEGFVKDIMLNKEETK 316
 DB 47 HRLDKIEDERNLHEDFVFMKTQRCNTGERSLSLNCETIKSFEGFVKDIMLNKEETK 106
 QY 317 KENSEFMOKGONPOIAAHVISEASSKTTSVLQWAEKGYTMSNNLVLTENGKQLTVKRQ 376
 DB 107 KENSEFMOKGONPOIAAHVISEASSKTTSVLQWAEKGYTMSNNLVLTENGKQLTVKRQ 166
 QY 377 GLYTYIAOVTFCSNREASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGOOSTHIG 436
 DB 167 GLYTYIAOVTFCSNREASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGOOSTHIG 226
 QY 437 GVFELOPGASVFNVTDPDSOVSHGTGFTSPGLTKL 471
 DB 227 GVFELOPGASVFNVTDPDSOVSHGTGFTSPGLTKL 261
 RESULT 6
 AAW71751
 ID AAW71751 standard; Protein: 261 AA.
 XX AAW71751;
 AC
 DT 08-DEC-1998 (first entry)
 XX
 DE Human CD40 ligand.
 XX
 KW Human; CD40 ligand; TNF receptor family; activated T cell;
 KW type 2 membrane glycoprotein; cell proliferation; differentiation;
 KW B cell.
 XX
 OS Homo sapiens.

XX US5817516-A.
 PN 06-OCT-1998.
 XX
 PD 28-APR-1995; 95US-0431055.
 XX
 PF 28-APR-1995; 95US-0431055.
 XX
 PR 28-APR-1994; 94US-0234580.
 XX
 PA (BOEHRINGER INGELHEIM PHARM INC.
 PI Castle B, Kehry M;
 DR WPI: 1998-556393/47.
 DR N-PSDB; AAV61063.
 XX
 PT Increased proliferation of B cells in culture - by incubating them
 PT in the presence of membrane-bound CD40 ligand
 XX
 PS Example 1: Fig 1; 37pp; English.
 CC
 CC The present sequence represents human CD40 ligand which is used in the
 CC method of the invention. The method has been developed for proliferating
 CC B cells to increase their number at least 100-fold. The method
 CC comprises: (a) providing high density, membrane bound CD40 ligand; and
 CC (b) culturing one or more B cells in the presence of this ligand. The
 CC culture results in a proliferation in the number of B cells of at least
 CC 100 fold. Also described is a method as above where the B cells are
 CC induced to differentiate into antibody-producing cells in the presence
 CC of one or more cytokines. The method can be used for stimulating B-cell
 CC proliferation in vitro or in vivo, e.g. for treating conditions in which
 CC B-cell proliferation and activation is suppressed. Eight rounds of
 CC division over six days can be achieved, corresponding to a 256-fold
 CC increase in cell numbers, which is a vast increase compared to previous
 CC culturing methods.
 CC
 SQ Sequence 261 AA:
 44.6%; Score 1110; DB 19; Length 261;
 Best Local Similarity 100.0%; Pred. No. 1.3e-73;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 257 HRLDKIEDERNLHEDFVFMKTQRCNTGERSLSLNCETIKSFEGFVKDIMLNKEETK 316
 DB 47 HRLDKIEDERNLHEDFVFMKTQRCNTGERSLSLNCETIKSFEGFVKDIMLNKEETK 106
 QY 317 KENSEFMOKGONPOIAAHVISEASSKTTSVLQWAEKGYTMSNNLVLTENGKQLTVKRQ 376
 DB 107 KENSEFMOKGONPOIAAHVISEASSKTTSVLQWAEKGYTMSNNLVLTENGKQLTVKRQ 166
 QY 377 GLYTYIAOVTFCSNREASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGOOSTHIG 436
 DB 167 GLYTYIAOVTFCSNREASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGOOSTHIG 226
 QY 437 GVFELOPGASVFNVTDPDSOVSHGTGFTSPGLTKL 471
 DB 227 GVFELOPGASVFNVTDPDSOVSHGTGFTSPGLTKL 261
 RESULT 7
 AAW41178
 ID AAW41178 standard; Protein: 261 AA.
 XX AAW41178;
 AC
 DT 13-MAY-1998 (first entry)
 XX
 DE CD40 ligand.
 XX
 KW Leucine zipper; fusion protein production; soluble oligomeric protein;
 KW heterologous mammalian type II transmembrane protein; activated T cell;

KW heterologous mammalian type I transmembrane protein; antibody production;
CD40-L; B-cell proliferation; CD27-L; lymphocyte antigen.
XX
XX Homo sapiens.
OS
XX US5716805-A.
PN
XX 10-FEB-1998.
PD
XX 18-MAY-1995; 95US-0446922.
PF
XX 18-MAY-1995; 95US-0446922.
PR 25-OCT-1991; 91US-0783707.
PR 05-DEC-1991; 91US-0805723.
PR 23-OCT-1992; 92US-0969703.
PR 13-AUG-1993; 93US-0107353.
XX
XX (IMMUNEX CORP.
PI Spriggs MK, Srinivasan S;
XX WPI: 1998-144799/13.
DR N-PSDB; AAV12852.
XX
XX Soluble oligomeric fusion proteins - comprising leucine zipper fused
PT to extracellular region of transmembrane protein
XX
XX Example 1: column 21-22; 21pp; English.
XX
XX This sequence represents the the human CD40 ligand (CD40-L).
CC This protein can be used in a fusion protein produced using the
CC method of the invention. The method is for preparing soluble oligomeric
CC protein by culturing a host cell transfected with a vector for the
CC fusion protein. The soluble oligomeric proteins comprise a leucine zipper
CC fused to the N terminus of the extracellular region of a heterologous
CC mammalian type II transmembrane protein or to the C terminus of the
CC extracellular region of a heterologous mammalian type I transmembrane
CC protein, where the leucine zipper is a peptide comprising at least part
CC of AAW41171 or AAW41172, optionally with conservative amino acid
CC substitutions, provided that the peptide trimerizes in solution. A
CC soluble fusion protein comprising the leucine zipper of AAW41171 linked
CC to the extracellular region of CD40-L (a type II transmembrane protein
CC that is found on activated T cells and acts as a ligand for the B-cell
CC antigen CD40) stimulates B-cell proliferation and antibody production in
CC a similar manner to membrane-bound CD40-L. A soluble fusion protein
CC comprising the leucine zipper of AAW41172 linked to the extracellular
CC region of CD27-L (a type II transmembrane protein that binds to the
CC lymphocyte antigen CD27) inhibits binding of CD27c (a fusion protein
CC comprising the extracellular region of CD27 and a human IgG1 Fc region)
CC to EBV-transformed B cells expressing CD27-L.
XX
XX Sequence 261 AA:
SQ

Query Match 44.6%; Score 1110; DB 19; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.3e-73;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

257 HRLDKIEDERNLHEDFVFMKTTORCNTGERSLSLNCCEIKSOFEGYKDIMLKEERK 316
|||||
47 hrrldkiedernlhedfvmktlqrcntgerslsllnceelsqfegfvdmlkeek 106
Db
317 KENSFEMOGDONPOIAAHYISEASSKTTSVLQNAEKGYTMSNNLVLTENGKOLTVKRO 376
|||||
107 kensfemogdqdpqiaahviseassktvslqnaekgytmsnnlvltengkqltvkrtq 166
Db
377 GLYIYIAQVTFCSNREASSQAPFIASICLKSPGFRERILRAANTHSSAKPCGOOSIHLG 436
|||||
167 glyiyiaqvtfcsnreassqapfiiasiclkspgfrerillraanthssakpcgqgsihlg 226
Db
437 GVFELOPGASVFNVTDPDSOVSHGTGTFSGCLKL 471
|||||
227 gvfeilpgasvfnvtdpsqvshgtgftsfgllkl 261
Db

RESULT 8
AA39938
ID AA39938 standard; Protein; 261 AA.
XX
XX AC
XX AAY39938;
XX
XX 13-DEC-1999 (first entry)
XX
XX Human CD40-L protein sequence.
XX
XX DE
XX CD40-L; CD40 receptor ligand; anti-human CD40-L monoclonal antibody;
KW binding inhibitor; trimeric CD40-L; anti-immunoglobulin M;
KW peripheral blood B cell; proliferation inhibitor.
XX
XX OS
XX Homo sapiens.
XX
XX US5961974-A.
XX
XX 05-OCT-1999.
XX
XX 24-MAY-1994; 94US-0249189.
XX
XX PF
XX 25-OCT-1991; 91US-0783707.
XX 05-DEC-1991; 91US-0805723.
XX 23-OCT-1992; 92US-0969703.
XX
XX (IMMUNEX CORP.
XX
XX Spriggs MK, Fanslow WC, Armitage RJ;
XX WPI: 1999-579604/49.
XX
XX N-PSDB; AA227525.
XX
XX Anti-human CD40-L ligand monoclonal antibodies -
XX
XX Disclosure: Fig 2; 59pp; English.
XX
XX This sequence represents the human CD40 receptor ligand (CD40-L). The
CC invention relates to anti-human CD40-L monoclonal antibodies M90 secreted
CC by hybridoma hCD40L-M90 (ATCC HB-12055) and M91 secreted by hybridoma
CC hCD40L-M91 (ATCC HB-12056). M90 and M91 inhibit CD40-L binding to CD40
CC and the ability of trimeric CD40-L and anti-immunoglobulin M to induce
CC proliferation of peripheral blood B cells.
XX
XX Sequence 261 AA:
SQ

Query Match 44.6%; Score 1110; DB 20; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.3e-73;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

257 HRLDKIEDERNLHEDFVFMKTTORCNTGERSLSLNCCEIKSOFEGYKDIMLKEERK 316
|||||
47 hrrldkiedernlhedfvmktlqrcntgerslsllnceelsqfegfvdmlkeek 106
Db
317 KENSFEMOGDONPOIAAHYISEASSKTTSVLQNAEKGYTMSNNLVLTENGKOLTVKRO 376
|||||
107 kensfemogdqdpqiaahviseassktvslqnaekgytmsnnlvltengkqltvkrtq 166
Db
377 GLYIYIAQVTFCSNREASSQAPFIASICLKSPGFRERILRAANTHSSAKPCGOOSIHLG 436
|||||
167 glyiyiaqvtfcsnreassqapfiiasiclkspgfrerillraanthssakpcgqgsihlg 226
Db
437 GVFELOPGASVFNVTDPDSOVSHGTGTFSGCLKL 471
|||||
227 gvfeilpgasvfnvtdpsqvshgtgftsfgllkl 261
Db

RESULT 9
AA25155
ID AA25155 standard; protein; 261 AA.

XX AAY25155;
 AC
 XX 27-AUG-1999 (first entry)
 DT
 XX Human soluble CD40L protein.
 DE
 XX CD40L; human; soluble; inhibitor; immune response; T-cell function;
 XX alloimmunization; immunotherapy; antibody response; model; PB; Th cell;
 XX peripheral blood lymphocytes; therapy; B cell; APC; CD40; T-helper cell;
 XX cytokine secretion; transfection-induced alloimmune response; anti-HLA;
 XX systemic lupus erythematosus; SLE; Sjogrens syndrome; Raynaud's syndrome;
 XX scleroderma myositis; type 1 diabetes; arthritis; rheumatoid arthritis;
 XX inflammatory bowel disease; uveitis; myasthenia gravis; allergy;
 XX multiple sclerosis; idiopathic thrombocytopenic purpura; neuroprotective;
 XX graft vs host disease; dermatological; immunosuppressive; antidiabetic;
 XX antiinflammatory; antirheumatic; antiarthritic; antiallergic.
 OS
 XX Homo sapiens.
 XX MO9927948-A2.
 XX 10-JUN-1999.
 XX 27-NOV-1998; 98WO-CA01105.
 XX 28-NOV-1997; 97CA-2223225.
 XX (CABL-) CANADIAN BLOOD SERVICES;
 XX
 XX Crow AR, Freedman J, Lazarus AH;
 XX MPI: 1999-404800/34.
 DR
 XX Use of recombinant human CD40L protein for treating immune diseases
 PT
 XX Claim 2; Page 41-42; 42pp; English.
 PS
 XX This invention describes a novel use of a soluble recombinant human CD40L
 XX (rhCD40L) protein or protein fragment (containing the active binding site
 XX with CD40) for inhibiting an immune response and T-cell function. The
 XX invention also describes (1) an immunodeficient mouse model of human
 XX alloimmunization for testing in vivo effects of an immunotherapy or
 XX inhibition of a human antibody response, where the mouse model is an
 XX immunodeficient mouse reconstituted with human peripheral blood
 XX lymphocytes (PB), from donors and (2) A method for inhibiting an immune
 XX response, or T-cell function, in a patient by administering a therapeutic
 XX amount of rhCD40L or functional fragment. The soluble recombinant CD40L
 XX active fragment competes B cell-(or antigen presenting cell (APC)-) CD40
 XX interaction with CD40L on the Th (T-helper) cells which disallows the Th
 XX cell to be activated to secrete cytokines (such as Th2 cytokines) which
 XX thus reduce the transfection-induced alloimmune response. The rhCD40L or
 XX its fragment is useful for inhibiting a human anti-HLA alloimmune
 XX response. Where T-cell function is inhibited the following diseases can
 XX be treated or prevented: systemic lupus erythematosus (SLE), Sjogrens
 XX syndrome, scleroderma myositis, Raynaud's syndrome, type 1 diabetes,
 XX arthritis and rheumatoid arthritis, inflammatory bowel disease, uveitis,
 XX myasthenia gravis, multiple sclerosis, idiopathic thrombocytopenic
 XX purpura and graft vs host disease, and allergies dependent on T-cells.
 XX The development of the model will allow detailed study of the mechanisms
 XX of alloimmunization and allow the development of new strategies for the
 XX modulation of human alloimmunization to blood cell antigens.
 XX Administration of a recombinant 18kDa-CD154 molecule can inhibit an
 XX alloimmune response. This molecule may have good therapeutic potential
 XX to inhibit human transfection-induced alloimmunization. The product of
 XX the invention has dermatological, immunosuppressive, antiinflammatory,
 XX antirheumatic, antiarthritic, antidiabetic, neuroprotective and
 XX antiallergic activity.
 CC
 CC Sequence 261 AA:

Query Match

44.6%; Score 1110; DB 20; Length 261;

Best Local Similarity 100.0%; Pred. No. 1.3e-73;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 257 HRRLDKIEDERNLHEDFVFKTTRQRCNTGERSLILNCEERKSGFEFVRYIMLKEETK 316
 DB 47 HRLDKIEDERNLHEDFVFKTTRQRCNTGERSLILNCEERKSGFEFVRYIMLKEETK 106
 QY 317 KENSFEMOKGQONPOIAAHVISEASSKTSYVLQMAEKGYTMSNNLTLENGKQUTVRO 376
 DB 107 KENSFEMKXGQNPQAIAHVISEASSKTSYVLQMAEKGYTMSNNLTLENGKQUTVRO 166
 QY 377 GLYVYAAQVTFECNSPEASSQAPFIASLCRSPRFRERILLRANTHSSAKPCGOOSIHLG 436
 DB 167 GLYVYAAQVTFECNSPEASSQAPFIASLCRSPRFRERILLRANTHSSAKPCGOOSIHLG 226
 QY 437 GVPEIQGASVFNVTDPSSQVSHGTGTFSGDLKL 471
 DB 227 GVPEIQGASVFNVTDPSSQVSHGTGTFSGDLKL 261

RESULT 10

AA96993
 ID AAY96993 standard; Protein; 261 AA.

AC AAY96993;

DT 31-OCT-2000 (first entry)

DE Human CD40 ligand.

KW CD40 ligand; CD40; T cell; T cell receptor; rearrangement; maturation;
 KW cell death inhibition; stress-induced; immunosuppressive; anti-thyroid;
 KW anti-inflammatory; anti-diabetic; anti-rheumatic; anti-anaemic;
 KW ophthalmological; anti-psoriatic; nephrotrophic; hepatotropic; virucide;
 KW dermatological; cytostatic.

OS Homo sapiens.

PN MO200039283-A1.

PD 06-JUL-2000.

PF 22-DEC-1999; 99WO-US30930.

PR 29-DEC-1998; 98US-0114106.

PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.

PI Newell MK, Wagner D, Newell E;

DR MPI: 2000-452387/39.

DR N-PSDB: AAA51745.

PT Inducing T cell receptor gene rearrangement for treating autoimmune
 PT diseases comprises contacting T cells with a CD40-binding agent
 PS
 PS Disclosure: Page 47; 50pp; English.

CC CD40 engagement on T cells has been used to induce T cell receptor
 CC rearrangement and enhance T cell affinity for a particular antigen. CD40
 CC engagement can be bought about by contacting CD40 with a CD40-binding
 CC agent, e.g. human CD40 ligand. The CD40-binding agents can also be used
 CC in methods for promoting T cell maturation, inhibiting T cell receptor
 CC rearrangement, inhibiting environmental stress-induced cell death,
 CC altering the specificity of a T cell towards an antigen, inducing T cell
 CC reactivity towards an antigen or enhancing environmental stress-induced
 CC cell death (all claimed). T cell affinity maturation towards a specific
 CC antigen can be inhibited, especially for a self-antigen in an autoimmune
 CC disease, which includes rheumatoid arthritis, uveitis, insulin-dependent
 CC diabetes mellitus, haemolytic anaemias, rheumatic fever, Crohn's disease,
 CC Guillain-Barre syndrome, psoriasis, thyroiditis, Grave's disease,
 CC myasthenia gravis, glomerulonephritis, autoimmune hepatitis or systemic
 CC lupus erythematosus. Inducing environmental stress-induced T cell death

CC is carried out in a cancerous T cell or a self-reactive T cell where the
CC environmental stress is a chemotherapeutic agent (claimed).
XX
XX Sequence 261 AA:

Query Match 44.6%; Score 1110; DB 21; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.3e-73;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 257 HRRLDKIDERNLHEDFVFWKTTORCNTGERSLSLNCCEIKSQEGFVKDMLNKEERK 316
DB 47 hrrldkiedernlhedfvmktlqrcntgerslslnceelsqegfvtkdmlnkeek 106
OY 317 KENSFEMOKGDNPOJIAAHVISEASSKTTSVLQMAEKGYTMSNNLVTLNKGKOLTVKRO 376
DB 107 kensfemqgdnqpjiaahviseassktstavlqwaekgytmsnnlvclengkqltvkrq 166
OY 377 GLYTYIAQVTFCSNREASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGQSIHLG 436
DB 167 glytyiaqvtfcsnreassqapfiaslclksprferillraanthssakpcgqsihlg 226
OY 437 GVFELOPGASVFVNVTDPQSVSHGTGFTSPGLKL 471
DB 227 gvfeiqpasvfvnvtldpqsvshgtgftspglkl 261

RESULT 11

AAB67612
ID AAB67612 standard; Protein; 261 AA.

AC AAB67612;

DT 29-MAY-2001 (first entry)

DE Amino acid sequence of human gp39 protein, a CD40 ligand.

XX gp39; CD40 ligand; osteoblast cell death; apoptosis; bone loss;
KM osteoporosis; osteonecrosis; inflammatory arthritis; estrogen loss;
KM ovariectomy; hysterectomy; lupus nephritis; Takayasu's arteritis;
KM Wegener's granulomatosis; nephritis; myositis; scleroderma;
KM thrombocytopenia; asthma; lung disease; cancer.

OS Homo sapiens.

XX WO200116180-A2.

XX 08-MAR-2001.

XX 24-AUG-2000; 2000WO-US23276.

XX 27-AUG-1999; 99US-0151250.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Ahuja SS, Bonewald LF;

XX WPI: 2001-169007/17.

XX N-PSDB: AAF55539.

PT CD40 agonist containing composition, used to reduce bone cell death or
PT apoptosis associated with osteoporosis, osteonecrosis and inflammatory
PT arthritis -

PS Claim 3; Page 113-114; 118pp; English.

XX The present sequence represents a gp39 protein. It is a CD40 ligand.
CC CD40 ligands are used for reducing osteoblast cell death or apoptosis,
CC and for treating or preventing bone loss in animals, preferably humans,
CC at risk of, or undergoing, bone loss. The bone loss is associated with
CC osteoporosis, osteonecrosis, inflammatory arthritis, post-menopausal
CC oestrogen loss, estrogen loss due to ovariectomy, total hysterectomy,
CC lupus nephritis, Takayasu's arteritis, Wegener's granulomatosis.

CC anti-glomerular basement membrane nephritis, myositis, scleroderma,
CC idiopathic autoimmune thrombocytopenia, asthma, a chronic obstructive
CC lung disease, nephrotic/nephritic syndrome, or cancer. They may also be
CC used to treat or prevent bone loss in a subject undergoing, or scheduled
CC for, an organ or bone marrow transplant.

XX Sequence 261 AA:

Query Match 44.6%; Score 1110; DB 22; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.3e-73;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 257 HRRLDKIDERNLHEDFVFWKTTORCNTGERSLSLNCCEIKSQEGFVKDMLNKEERK 316
DB 47 hrrldkiedernlhedfvmktlqrcntgerslslnceelsqegfvtkdmlnkeek 106
OY 317 KENSFEMOKGDNPOJIAAHVISEASSKTTSVLQMAEKGYTMSNNLVTLNKGKOLTVKRO 376
DB 107 kensfemqgdnqpjiaahviseassktstavlqwaekgytmsnnlvclengkqltvkrq 166
OY 377 GLYTYIAQVTFCSNREASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGQSIHLG 436
DB 167 glytyiaqvtfcsnreassqapfiaslclksprferillraanthssakpcgqsihlg 226
OY 437 GVFELOPGASVFVNVTDPQSVSHGTGFTSPGLKL 471
DB 227 gvfeiqpasvfvnvtldpqsvshgtgftspglkl 261

RESULT 12

AAB37806
ID AAB37806 standard; Protein; 261 AA.

AC AAB37806;

DT 23-FEB-2001 (first entry)

DE Human CD40 ligand sequence.

XX Human; CD40 ligand; antiviral; anti-HIV; CD40 stimulant;

XX human immunodeficiency virus; HIV; cancer; organ transplantation.

XX Homo sapiens.

XX WO200066155-A1.

XX 09-NOV-2000.

XX 28-APR-2000; 2000WO-US11734.

XX 30-APR-1999; 99US-0131730.

XX (JLOL-) LA JOLLA INST ALLERGY & IMMUNOLOGY.

XX Sarawar SR, Schoenberger SP;

XX WPI: 2001-024740/03.

PT Method for preventing latent virus reactivation or controlling virus
PT replication by administration of antibodies or similar reagents which
PT stimulate the CD40 molecule -

PS Disclosure; Page 16; 36pp; English.

XX The present sequence is a human CD40 ligand. It may be used in a method
CC for preventing latent virus reactivation or controlling virus
CC replication. The method comprises administering a composition capable
CC of binding to a cell membrane expressed CD40, where the binding of the
CC composition to the CD40 on the surface of the cell generates a
CC stimulatory signal to the cell. The method is useful for treating
CC immunocompromised patients, e.g. infected with human immunodeficiency
CC virus (HIV), or immunosuppressed patients, e.g. due to infections or

CC illness, or as a side effect of treatments (such as radiation or cancer
 CC therapy), or due to tissue or organ transplantation. The method does
 CC not have the levels of toxicity seen following administration of
 CC conventional antiviral drugs.
 XX
 SQ Sequence 261 AA;

Query Match 44.68; Score 1110; DB 22; Length 261;
 Best Local Similarity 100.0%; Pred. No. 1.3e-73;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 HRLDKIEDERNLHEDVFEMKTIQRCNTGNSLSLNCHEIKSQEGYKIDMLNKEETK 316
 |||||||
 DB 47 hrrldkiedernlhedvfemkltqrcnlgerslsllnceelksqfegfvkdmlnkeek 106
 QY 317 KENSFEMOKGQONPOIAAHVISEASSKTTSVLQMAEKGYTMSNNLYLTENKQOLTVKQ 376
 |||||||
 DB 107 kensfemokgqonpoiaahviseasskttsvlqmaekgytmsnnlyltengkqltvkrq 166
 QY 377 GLYITTAQVTFGCSNREASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGQOSIHG 436
 |||||||
 DB 167 glyityaqvtfcsnreassqapfiastclksprferillraanthssakpcgqsinhg 226
 QY 437 GVFELOPGASVFYNNVDPQOVSHGTGTFSLKL 471
 |||||||
 DB 227 gvfelqpgasvfyvnnvdpsqvsngtftslgllkl 261

RESULT 13

AAW09122 standard; Protein; 294 AA.

AC AAW09122;

DT 24-SEP-1997 (first entry)

DE CD40 ligand/zipper domain fusion protein mutant 41.

KW CD40 ligand; membrane bound glycoprotein; B cell proliferation;
 antibody secretion; immunoglobulin E; cytokine; CD40L; mutein;

KM oligomerisation domain; fusion protein; dimer; trimer.

XX Chimeric - Homo sapiens.

OS Chimeric - Saccharomyces cerevisiae.

OS Synthetic.

PH Key Location/Qualifiers
 FT Domain 1..33
 /label= leucine zipper_15M_116T

FT Misc-difference 5 /note= "Mutant version of yeast GCN4 leucine zipper"

FT MISC-difference 16 /note= "Wild-type Ile has been replaced by Met"

FT Region 34..294 /note= "Wild-type Ile has been replaced by Thr"

FT /label= CD40L

PN WO9640918-A2.

PD 19-DEC-1996.

PF 06-JUN-1996; 96WO-US09632.

PR 07-JUN-1995; 95US-0484624.

PR 07-JUN-1995; 95US-0477733.

PA (IMMUNEX CORP.

XX Armilace RJ, Fanslow WC, Gibson MG, Springs MK;

PI Srinivasan S;

FT WPI; 1597-052320/05.

XX New CD40 ligand mutein with higher CD40 affinity than native ligand
 PT - useful in binding assays, and for therapy of disorders and
 PT diseases involving low levels of B cells and antibody secretion
 XX
 PS Example 4; Page -; 31pp; English.

CC This sequence represents a mutant version of human CD40 ligand/
 CC zipper domain fusion protein which is able to bind CD40 in a solid
 CC phase binding assay. The random mutations were generated by PCR
 CC misincorporation into yeast expression constructs and mutants were
 CC selected based on an apparent increase in secretion.
 CC (Note: The present sequence does not appear in the specification;
 CC it has been produced using the sequences of the leucine zipper and
 CC wild-type CD40L which are given on page 23 and pages 20-21,
 CC respectively).

XX Sequence 294 AA;

Query Match 44.68; Score 1110; DB 18; Length 294;
 Best Local Similarity 100.0%; Pred. No. 1.5e-73;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 HRLDKIEDERNLHEDVFEMKTIQRCNTGNSLSLNCHEIKSQEGYKIDMLNKEETK 316
 |||||||
 DB 80 hrrldkiedernlhedvfemkltqrcnlgerslsllnceelksqfegfvkdmlnkeek 139
 QY 317 KENSFEMOKGQONPOIAAHVISEASSKTTSVLQMAEKGYTMSNNLYLTENKQOLTVKQ 376
 |||||||
 DB 140 kensfemokgqonpoiaahviseasskttsvlqmaekgytmsnnlyltengkqltvkrq 199
 QY 377 GLYITTAQVTFGCSNREASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGQOSIHG 436
 |||||||
 DB 200 glyityaqvtfcsnreassqapfiastclksprferillraanthssakpcgqsinhg 259
 QY 437 GVFELOPGASVFYNNVDPQOVSHGTGTFSLKL 471
 |||||||
 DB 260 gvfelqpgasvfyvnnvdpsqvsngtftslgllkl 294

RESULT 14

AAW09119 standard; Protein; 294 AA.

AC AAW09119;

DT 24-SEP-1997 (first entry)

DE CD40 ligand/zipper domain fusion protein mutant 14.

KW CD40 ligand; membrane bound glycoprotein; B cell proliferation;
 antibody secretion; immunoglobulin E; cytokine; CD40L; mutein;

KM oligomerisation domain; fusion protein; dimer; trimer.

XX Chimeric - Homo sapiens.

OS Chimeric - Saccharomyces cerevisiae.

OS Synthetic.

PH Key Location/Qualifiers
 FT Domain 1..33
 /label= leucine zipper_112N

FT Misc-difference 12 /note= "Mutant version of yeast GCN4 leucine zipper"

FT Region 34..294 /note= "Wild-type Ile has been replaced by Asn"

FT /label= CD40L_K260N

FT MISC-difference 293 /note= "Wild-type Lys has been replaced by Asn"

PN WO9640918-A2.

PD 19-DEC-1996.
 XX 06-JUN-1996; 96WO-US09632.
 XX 07-JUN-1995; 95US-0484624.
 PR 07-JUN-1995; 95US-0477733.
 XX (IMMUNEX CORP.
 PA Amltage RJ, Fanslow WC, Gibson MG, Spriggs MK;
 PI Srinivasan S;
 DR WPI: 1997-052320/05.
 XX
 XX New CD40 ligand mutein with higher CD40 affinity than native ligand
 PT - useful in binding assays, and for therapy of disorders and
 PT diseases involving low levels of B cells and antibody secretion
 XX
 XX Example 4; Page -: 31pp; English.
 XX
 CC This sequence represents a mutant version of human CD40 ligand/
 CC zipper domain fusion protein which is able to bind CD40 in a solid
 CC phase binding assay. The random mutations were generated by PCR
 CC misincorporation into yeast expression constructs and mutants were
 CC selected based on an apparent increase in secretion.
 CC (Note: The present sequence does not appear in the specification;
 CC it has been produced using the sequences of the leucine zipper and
 CC wild-type CD40L which are given on page 23 and pages 20-21,
 CC respectively).
 CC
 XX Sequence 294 AA:
 SO

Query Match 44.4%; Score 1105; DB 18; Length 294;
 Best Local Similarity 99.5%; Pred. No. 3,4e-73;
 Matches 214; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 257 HRLDKIEDERNLHEDFVFMKTIORCMTGERSLSLNCSEIKSOEGFYKDIMLKEETK 316
 DB 80 hrrldkiedernlhedvfkmktiorcmgterslslnceelsksgtegytkdimlneek 139
 QY 317 KENFEMQKGDQNPQIAAHVISEASSTKTSVLQNAEKGYTMSNNLVTLNKGQLTVKRO 376
 DB 140 kensfemqgdqnpqiaahviseasstktsvlywaekgytmsnnlvclengkqltvkrq 199
 QY 377 GLYIYAQVTFCSNREASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGQGSIHG 436
 DB 200 glylyiaqvtfcsnreassqapfiaslclksgrferillraanthssakpcgqgsihg 259
 QY 437 GVFEIQPGASVFNVTDPDSOVSHGTGFTSGFLKL 471
 DB 260 gvfeiqpgasvfnvtdpsqvsngtftsgflkl 294

RESULT 15
 AAM09121
 ID AAM09121 standard; Protein: 294 AA.
 XX
 AC AAM09121;
 XX
 DT 24-SEP-1997 (first entry)
 XX
 DE CD40 ligand/zipper domain fusion protein mutant 32.
 XX
 KW CD40 ligand; membrane bound glycoprotein; B cell proliferation;
 KW antibody secretion; immunoglobulin E; cytokine; CD40L; mutein;
 KW oligomerization domain; fusion protein; dimer; trimer.
 XX
 OS Chimeric - Homo sapiens.
 OS Chimeric - Saccharomyces cerevisiae.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH

FT Domain 1.33
 FT /label= leucine_zipper_112N
 FT /note= "Mutant version of yeast GCN4 leucine zipper"
 FT Misc-difference 12
 FT /note= "Wild-type Ile has been replaced by Asn"
 FT Region 34.294
 FT /label= CD40L_Q121P
 FT /note= "Mutant version of CD40 ligand"
 FT Misc-difference 154
 FT /note= "Wild-type Gln has been replaced by Pro"
 XX
 PN W09640918-A2.
 XX
 XX 19-DEC-1996.
 XX
 PD 06-JUN-1996; 96WO-US09632.
 XX
 PF 07-JUN-1995; 95US-0484624.
 PR 07-JUN-1995; 95US-0477733.
 XX
 XX (IMMUNEX CORP.
 PA Amltage RJ, Fanslow WC, Gibson MG, Spriggs MK;
 PI Srinivasan S;
 DR WPI: 1997-052320/05.
 XX
 XX New CD40 ligand mutein with higher CD40 affinity than native ligand
 PT - useful in binding assays, and for therapy of disorders and
 PT diseases involving low levels of B cells and antibody secretion
 XX
 XX Example 4; Page -: 31pp; English.
 XX
 CC This sequence represents a mutant version of human CD40 ligand/
 CC zipper domain fusion protein which is able to bind CD40 in a solid
 CC phase binding assay. The random mutations were generated by PCR
 CC misincorporation into yeast expression constructs and mutants were
 CC selected based on an apparent increase in secretion.
 CC (Note: The present sequence does not appear in the specification;
 CC it has been produced using the sequences of the leucine zipper and
 CC wild-type CD40L which are given on page 23 and pages 20-21,
 CC respectively).
 CC
 XX Sequence 294 AA:
 SO

Query Match 44.4%; Score 1104; DB 18; Length 294;
 Best Local Similarity 99.5%; Pred. No. 4e-73;
 Matches 214; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 257 HRLDKIEDERNLHEDFVFMKTIORCMTGERSLSLNCSEIKSOEGFYKDIMLKEETK 316
 DB 80 hrrldkiedernlhedvfkmktiorcmgterslslnceelsksgtegytkdimlneek 139
 QY 317 KENFEMQKGDQNPQIAAHVISEASSTKTSVLQNAEKGYTMSNNLVTLNKGQLTVKRO 376
 DB 140 kensfemqgdqnpqiaahviseasstktsvlywaekgytmsnnlvclengkqltvkrq 199
 QY 377 GLYIYAQVTFCSNREASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGQGSIHG 436
 DB 200 glylyiaqvtfcsnreassqapfiaslclksgrferillraanthssakpcgqgsihg 259
 QY 437 GVFEIQPGASVFNVTDPDSOVSHGTGFTSGFLKL 471
 DB 260 gvfeiqpgasvfnvtdpsqvsngtftsgflkl 294

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Tue Jul 3 16:26:03 2001

us-09-454-223-2.rag

Page 10

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OM protein - protein search, using sw model

Run on: July 3, 2001, 16:13:43 : Search time 17.98 Seconds

(without alignments)
527.704 Million cell updates/sec

Title: US-09-454-223-2

Perfect score: 2487
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Sequence:

BLOSUM62
Gapop 10.0 , Gapext 0.5

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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2: /cgn2_6/ptodata/2/1aa/5b.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1110	44.6	261	1	US-07-940-605A-2
2	1110	44.6	261	1	US-08-184-422-8
3	1110	44.6	261	1	US-08-360-823A-2
4	1110	44.6	261	1	US-08-446-922-4
5	1110	44.6	261	2	US-08-431-055-4
6	1110	44.6	261	2	US-08-690-096-2
7	1110	44.6	261	2	US-08-249-189-12
8	1110	44.6	261	2	US-08-484-624A-12
9	1110	44.6	261	2	US-08-477-733B-12
10	1110	44.6	261	3	US-08-763-995-2
11	1110	44.6	261	3	US-09-088-913A-12
12	1110	44.6	261	3	US-08-589-771B-8
13	1110	44.6	261	5	PCT-US93-1003A-4
14	1094.5	44.0	273	1	US-08-446-922-11
15	1094.5	44.0	273	1	US-08-249-189-21
16	1094.5	44.0	273	2	US-08-484-624A-21
17	1094.5	44.0	273	2	US-08-477-733B-21
18	1094.5	44.0	273	3	US-09-088-913A-21
19	1089	43.8	473	2	US-08-249-189-16
20	1089	43.8	473	2	US-08-484-624A-16
21	1089	43.8	473	3	US-08-477-733B-16
22	1089	43.8	473	3	US-09-088-913A-16
23	831	33.4	260	2	US-08-446-922-6
24	831	33.4	260	2	US-08-249-189-2
25	831	33.4	260	2	US-08-484-624A-2
26	831	33.4	260	2	US-08-477-733B-2
27	831	33.4	260	3	US-09-088-913A-2

28	831	33.4	260	5	PCT-US93-1003A-6	Sequence 6, Appl
29	829.5	33.4	351	4	US-09-011-735-1	Sequence 1, Appl
30	827	33.3	260	2	US-08-431-055-2	Sequence 2, Appl
31	812	33.6	280	2	US-08-249-189-23	Sequence 23, Appl
32	812	33.6	280	2	US-08-484-624A-23	Sequence 23, Appl
33	812	33.6	280	2	US-08-477-733B-23	Sequence 23, Appl
34	812	32.6	280	3	US-09-088-913A-23	Sequence 23, Appl
35	766	30.8	149	3	US-08-584-031-16	Sequence 16, Appl
36	755	30.4	151	1	US-07-940-605A-3	Sequence 3, Appl
37	755	30.4	151	2	US-08-690-096-3	Sequence 3, Appl
38	652	26.2	171	4	US-09-011-735-2	Sequence 2, Appl
39	567	22.8	151	1	US-07-940-605A-4	Sequence 4, Appl
40	567	22.8	151	2	US-08-690-096-4	Sequence 4, Appl
41	481.5	19.4	1057	3	US-08-931-820-1	Sequence 1, Appl
42	474.5	19.1	1057	3	US-08-931-820-4	Sequence 4, Appl
43	474.5	19.1	1341	4	US-08-963-825-18	Sequence 18, Appl
44	473.5	19.0	1060	3	US-08-931-820-3	Sequence 3, Appl
45	473.5	19.0	1418	4	US-08-963-825-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-07-940-605A-2
Sequence 2, Application US/07940605A
Patent No. 5540926
GENERAL INFORMATION:
APPLICANT: ARUFFO, ALEJANDRO
APPLICANT: HOLLEBAUGH, DIANE
APPLICANT: LEDBETTER, JEFFREY A.
TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/940,605A
FILING DATE: 04-SEP-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-184
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-940-605A-2

Query Match 44.6% Score 1110 DB 1 Length 261:
Best Local Similarity 100.0% Pred. No. 3.5e+79:
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0:

OY 257 HRRLDKIEBRNLHEDVFEMKTTORCNTGERSLSLNKEEIKSOFGFYKDKIMLNKEETK 316
DB 47 HRRLDKIEBRNLHEDVFEMKTTORCNTGERSLSLNKEEIKSOFGFYKDKIMLNKEETK 106

OY 317 KENEFEMOKGDNQPOIAAHVISEASSKTTSVLQMAEKGYTMSNNLVTLNGKOLTVKRO 376
DB 107 KENEFEMOKGDNQPOIAAHVISEASSKTTSVLQMAEKGYTMSNNLVTLNGKOLTVKRO 166
OY 377 GLYYIAQVTFCSNREASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGQOSIHLG 436
DB 167 GLYYIAQVTFCSNREASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGQOSIHLG 226
OY 437 GFVELQPGASVFNVTDPDSQVSHGTGFTSFGLLKL 471
DB 227 GFVELQPGASVFNVTDPDSQVSHGTGFTSFGLLKL 261

RESULT 2

US-08-184-422-8
Sequence 8, Application US/08184422
Patent No. 5585321
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: DAVISON, BARRY
APPLICANT: FANSLAW, WILLIAM
APPLICANT: KENSHAW, BLAIR
APPLICANT: SPRIGGS, MELANIE
APPLICANT: WIDMER, MICHAEL
TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS
TITLE OF INVENTION: IN A CD40 LIGAND GENE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple Macintosh
SOFTWARE: MS Word for Apple 5.1, Version 2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,422
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/009,258
FILING DATE: 01/22/93
ATTORNEY/AGENT INFORMATION:
NAME: PERKINS, PATRICIA ANNE
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2818-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-184-422-8

Query Match 44.6%; Score 1110; DB 1; Length 261;
Best Local Similarity 100.0%; Pred. No. 3.5e-79;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 257 HRLDKIEDERNLHEDFVFMKTIORCNTGERSLSLNCSEIKSOEFGFKDMLNKEETK 316
DB 47 HRLDKIEDERNLHEDFVFMKTIORCNTGERSLSLNCSEIKSOEFGFKDMLNKEETK 106
OY 317 KENEFEMOKGDNQPOIAAHVISEASSKTTSVLQMAEKGYTMSNNLVTLNGKOLTVKRO 376
DB 227 GFVELQPGASVFNVTDPDSQVSHGTGFTSFGLLKL 261

DB 107 KENEFEMOKGDNQPOIAAHVISEASSKTTSVLQMAEKGYTMSNNLVTLNGKOLTVKRO 166
OY 377 GLYYIAQVTFCSNREASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGQOSIHLG 436
DB 167 GLYYIAQVTFCSNREASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGQOSIHLG 226
OY 437 GFVELQPGASVFNVTDPDSQVSHGTGFTSFGLLKL 471
DB 227 GFVELQPGASVFNVTDPDSQVSHGTGFTSFGLLKL 261

RESULT 3

US-08-360-923A-2
Sequence 2, Application US/08360923A
Patent No. 5674492
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: LONGO, DAN L.
APPLICANT: MURPHY, WILLIAM
TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING
TITLE OF INVENTION: DISEASE CHARACTERIZED BY NEOPLASTIC CELLS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple Macintosh
SOFTWARE: Microsoft Word for Macintosh, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,923A
FILING DATE: December 21, 1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/172,664
FILING DATE: December 23, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2818-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-360-923A-2

Query Match 44.6%; Score 1110; DB 1; Length 261;
Best Local Similarity 100.0%; Pred. No. 3.5e-79;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 257 HRLDKIEDERNLHEDFVFMKTIORCNTGERSLSLNCSEIKSOEFGFKDMLNKEETK 316
DB 47 HRLDKIEDERNLHEDFVFMKTIORCNTGERSLSLNCSEIKSOEFGFKDMLNKEETK 106
OY 317 KENEFEMOKGDNQPOIAAHVISEASSKTTSVLQMAEKGYTMSNNLVTLNGKOLTVKRO 376
DB 107 KENEFEMOKGDNQPOIAAHVISEASSKTTSVLQMAEKGYTMSNNLVTLNGKOLTVKRO 166
OY 377 GLYYIAQVTFCSNREASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGQOSIHLG 436

Db 167 GLYIYIAOVTFCSNRASSQAPFIASLCLKSPGFRERILLRAANTHSSAKPCGQOSIHIG 226
Qy 437 GFVELQPGASVFNVTDPQSVSHGTGFTSGLKL 471
Db 227 GFVELQPGASVFNVTDPQSVSHGTGFTSGLKL 261

RESULT 4

US-08-446-922-4
Sequence 4, Application US/08446922
Patent No. 5718605
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanle
APPLICANT: Sriivasan, Subhashini
TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,922
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 08/107,353
FILING DATE: 08-13-93
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 1003-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-446-922-4

Query Match 44.6%; Score 1110; DB 1; Length 261;
Best Local Similarity 100.0%; Pred. No. 3.5e-79;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 257 HRLDKIEDERLHEDFVFMKTIORCNTGERSLSLNCCEIKSQFEGFVKDMLNKEETK 316
Db 47 HRLDKIEDERLHEDFVFMKTIORCNTGERSLSLNCCEIKSQFEGFVKDMLNKEETK 106
Qy 317 KENSFEMKGDONPOIAAHVISEASSKTTSVLQMAEKGYTMSNNLVTLNKGKOLTVKRO 376
Db 107 KENSFEMKGDONPOIAAHVISEASSKTTSVLQMAEKGYTMSNNLVTLNKGKOLTVKRO 166
Qy 377 GLYIYIAOVTFCSNRASSQAPFIASLCLKSPGFRERILLRAANTHSSAKPCGQOSIHIG 436
Db 167 GLYIYIAOVTFCSNRASSQAPFIASLCLKSPGFRERILLRAANTHSSAKPCGQOSIHIG 226
Qy 437 GFVELQPGASVFNVTDPQSVSHGTGFTSGLKL 471
Db 227 GFVELQPGASVFNVTDPQSVSHGTGFTSGLKL 261

RESULT 5

US-08-431-055-4
Sequence 4, Application US/08431055
Patent No. 5817516
GENERAL INFORMATION:
APPLICANT: KEHR, MERILYN R
APPLICANT: CASTLE, BRIAN E
TITLE OF INVENTION: METHODS FOR PROLIFERATING AND
TITLE OF INVENTION: DIFFERENTIATING B CELLS, AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 100 NEW YORK AVE. N.W. SUITE 600
CITY: WASHINGTON
STATE: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,055
FILING DATE: 28-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/234,580
FILING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 1011.1030000/RAM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-431-055-4

Query Match 44.6%; Score 1110; DB 2; Length 261;
Best Local Similarity 100.0%; Pred. No. 3.5e-79;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 257 HRLDKIEDERLHEDFVFMKTIORCNTGERSLSLNCCEIKSQFEGFVKDMLNKEETK 316
Db 47 HRLDKIEDERLHEDFVFMKTIORCNTGERSLSLNCCEIKSQFEGFVKDMLNKEETK 106
Qy 317 KENSFEMKGDONPOIAAHVISEASSKTTSVLQMAEKGYTMSNNLVTLNKGKOLTVKRO 376
Db 107 KENSFEMKGDONPOIAAHVISEASSKTTSVLQMAEKGYTMSNNLVTLNKGKOLTVKRO 166
Qy 377 GLYIYIAOVTFCSNRASSQAPFIASLCLKSPGFRERILLRAANTHSSAKPCGQOSIHIG 436
Db 167 GLYIYIAOVTFCSNRASSQAPFIASLCLKSPGFRERILLRAANTHSSAKPCGQOSIHIG 226
Qy 437 GFVELQPGASVFNVTDPQSVSHGTGFTSGLKL 471
Db 227 GFVELQPGASVFNVTDPQSVSHGTGFTSGLKL 261

RESULT 6

US-08-690-096-2
Sequence 2, Application US/08690096
Patent No. 5945513
GENERAL INFORMATION:
APPLICANT: ARUFFO, ALEJANDRO

APPLICANT: HOLLENBAUGH, DIANE
APPLICANT: LEDBETTER, JEFFREY A.
TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,096
FILING DATE: 31-JUL-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/940,605
FILING DATE: 04-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-184
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9050
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-690-096-2

Query Match 44.6%; Score 1110; DB 2; Length 261;
Best Local Similarity 100.0%; Pred. No. 3.5e-79;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 HRLDKIEDENLHEDFVFMKTICRCNTGERSLSLNCCEIKSQFEGVXKDIMLNKEETK 316
DB 47 HRLDKIEDENLHEDFVFMKTICRCNTGERSLSLNCCEIKSQFEGVXKDIMLNKEETK 106
QY 317 KENSFEQKGDONPOIAHAHVISEASSKTSVLMQAEKGYTMSNNLVTLNGKQLTVKRO 376
DB 107 KENSFEQKGDONPOIAHAHVISEASSKTSVLMQAEKGYTMSNNLVTLNGKQLTVKRO 166
QY 377 GLYYIAQVTFCSNRRASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGOOSIHLG 436
DB 167 GLYYIAQVTFCSNRRASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGOOSIHLG 226
QY 437 GFVELQPGASVFVNTDPSQVSHGTGTFSGLLKL 471
DB 227 GFVELQPGASVFVNTDPSQVSHGTGTFSGLLKL 261

RESULT 7
US-08-249-139-12
Sequence 12, Application US/08249189
Patent No. 5961974
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
TITLE OF INVENTION: NOVEL CYTOKINE
NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1a
SOFTWARE: Microsoft Word for Apple, version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/249,189
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-249-189-12

Query Match 44.6%; Score 1110; DB 2; Length 261;
Best Local Similarity 100.0%; Pred. No. 3.5e-79;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 HRLDKIEDENLHEDFVFMKTICRCNTGERSLSLNCCEIKSQFEGVXKDIMLNKEETK 316
DB 47 HRLDKIEDENLHEDFVFMKTICRCNTGERSLSLNCCEIKSQFEGVXKDIMLNKEETK 106
QY 317 KENSFEQKGDONPOIAHAHVISEASSKTSVLMQAEKGYTMSNNLVTLNGKQLTVKRO 376
DB 107 KENSFEQKGDONPOIAHAHVISEASSKTSVLMQAEKGYTMSNNLVTLNGKQLTVKRO 166
QY 377 GLYYIAQVTFCSNRRASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGOOSIHLG 436
DB 167 GLYYIAQVTFCSNRRASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGOOSIHLG 226
QY 437 GFVELQPGASVFVNTDPSQVSHGTGTFSGLLKL 471
DB 227 GFVELQPGASVFVNTDPSQVSHGTGTFSGLLKL 261

RESULT 8
US-08-484-624A-12
Sequence 12, Application US/08484624A
Patent No. 5962406
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE

APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
APPLICANT: MORRIS, ARVIA E.
APPLICANT: MCGREM, JEFFERY
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple Macintosh
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,624A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,733
FILING DATE: June 07, 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-484-624A-12

Query Match 44.6%; Score 1110; DB 2; Length 261;
Best Local Similarity 100.0%; Pred. No. 3.5e-79;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 HRRDKIEDERNLHEDFVFMKTQRCNTGERSLSLNCCEIKSQFEGVVKDMLNKEERK 316
DB 47 HRRDKIEDERNLHEDFVFMKTQRCNTGERSLSLNCCEIKSQFEGVVKDMLNKEERK 106
QY 317 KENSFEMOGDONPQIAAHVISEASSTTSVLQWAEKGYTMSNNLVTLENGKQLTVKRO 376
DB 107 KENSFEMOGDONPQIAAHVISEASSTTSVLQWAEKGYTMSNNLVTLENGKQLTVKRO 166
QY 377 GLYIYAAQVTFCSNRRASSQAPFIASGLKSPGFERILLRAANTHSASAKPCGQOSIHG 436
DB 167 GLYIYAAQVTFCSNRRASSQAPFIASGLKSPGFERILLRAANTHSASAKPCGQOSIHG 226
QY 437 GVFEIOPGASVFNVTDPQSVSHGTGTSGFLKL 471
DB 227 GVFEIOPGASVFNVTDPQSVSHGTGTSGFLKL 261

RESULT 9
US-08-477-733B-12
Sequence 12, Application US/08477733B
Patent No. 5981724
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: FANSLAW, WILLIAM
APPLICANT: SPRIGGS, MELANIE
APPLICANT: SRINIVASAN, SUBHASHINI
APPLICANT: GIBSON, MARYLOU
APPLICANT: MORRIS, ARVIA E.
APPLICANT: MCGREM, JEFFERY
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple Macintosh
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,733B
FILING DATE: June 07, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,189
FILING DATE: May 24, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-733B-12

Query Match 44.6%; Score 1110; DB 2; Length 261;
Best Local Similarity 100.0%; Pred. No. 3.5e-79;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 HRRDKIEDERNLHEDFVFMKTQRCNTGERSLSLNCCEIKSQFEGVVKDMLNKEERK 316
DB 47 HRRDKIEDERNLHEDFVFMKTQRCNTGERSLSLNCCEIKSQFEGVVKDMLNKEERK 106
QY 317 KENSFEMOGDONPQIAAHVISEASSTTSVLQWAEKGYTMSNNLVTLENGKQLTVKRO 376

Db 107 KENSFEMOKGDONPOIAAHVISEASSKTTSVLQWAEKGYTMSNNLVTLLENGKOLTVRKQ 166
QY 377 GLYYIAQVTECSNREASSQAPFIASLCLKSPGERILLRAANTHSSAKPCGOOSIHLG 436
Db 167 GLYYIAQVTECSNREASSQAPFIASLCLKSPGERILLRAANTHSSAKPCGOOSIHLG 226
QY 437 GVFELOPGASVFNVTDPDSOVSHGTGTFSGLLKL 471
Db 227 GVFELOPGASVFNVTDPDSOVSHGTGTFSGLLKL 261

RESULT 10

US-08-763-995-2
; Sequence 2, Application US/08763995
; Patent No. 6017527
; GENERAL INFORMATION:
; APPLICANT: MARASKOVSKY, EUGENE
; TITLE OF INVENTION: METHOD OF ACTIVATING DENDRITIC CELLS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Macintosh, Version #6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/763,995
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/677,762
; FILING DATE: 10 JUL 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2845-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 261 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-763-995-2

Query Match 44.6%; Score 1110; DB 3; Length 261;
Best Local Similarity 100.0%; Pred. No. 3.5e-79;

Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 HRLDKIEDERNLHEDVFMKTIORCNTGERSLSLNCSEIKSOEGFVKDMLNKEETK 316
Db 47 HRLDKIEDERNLHEDVFMKTIORCNTGERSLSLNCSEIKSOEGFVKDMLNKEETK 106
QY 317 KENSFEMOKGDONPOIAAHVISEASSKTTSVLQWAEKGYTMSNNLVTLLENGKOLTVRKQ 376
Db 107 KENSFEMOKGDONPOIAAHVISEASSKTTSVLQWAEKGYTMSNNLVTLLENGKOLTVRKQ 166
QY 377 GLYYIAQVTECSNREASSQAPFIASLCLKSPGERILLRAANTHSSAKPCGOOSIHLG 436
Db 167 GLYYIAQVTECSNREASSQAPFIASLCLKSPGERILLRAANTHSSAKPCGOOSIHLG 226
QY 437 GVFELOPGASVFNVTDPDSOVSHGTGTFSGLLKL 471

Db 227 GVFELOPGASVFNVTDPDSOVSHGTGTFSGLLKL 261

RESULT 11

US-09-088-913A-12
; Sequence 12, Application US/09088913A
; Patent No. 6087329
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; APPLICANT: MORRIS, ARVIA E.
; APPLICANT: MCGREW, JEFFERY
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/088,913A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,624
; FILING DATE:
; APPLICATION NUMBER: 08/477,733
; FILING DATE: June 07, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,703
; FILING DATE: October 23, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/805,723
; FILING DATE: December 5, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/783,707
; FILING DATE: October 25, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2802-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2065870430
; TELEFAX: 2065870606
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 261 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-088-913A-12

Query Match 44.6%; Score 1110; DB 3; Length 261;
Best Local Similarity 100.0%; Pred. No. 3.5e-79;

Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 HRLDKIEDERNLHEDVFMKTIORCNTGERSLSLNCSEIKSOEGFVKDMLNKEETK 316
Db 47 HRLDKIEDERNLHEDVFMKTIORCNTGERSLSLNCSEIKSOEGFVKDMLNKEETK 106
QY 317 KENSFEMOKGDONPOIAAHVISEASSKTTSVLQWAEKGYTMSNNLVTLLENGKOLTVRKQ 376

Db 107 KENEFEMKGDONPOIAAHVISEASSKTTISVLQMAEKGYTMSNNLVLENKQOLTVKRO 166
OY 377 GLYIYAQVTFPCSNREASSQAPFIASLCLKSPGFERILLRANANTHSSAKPCGOOSIHG 436
Db 167 GLYIYAQVTFPCSNREASSQAPFIASLCLKSPGFERILLRANANTHSSAKPCGOOSIHG 226
OY 437 GFVELQPGASVFVNVTDPQSVSHGTGFTSFGLLKL 471
Db 227 GFVELQPGASVFVNVTDPQSVSHGTGFTSFGLLKL 261

RESULT 12
US-08-589-771B-8
Sequence 8, Application US/08589771B
Patent No. 6106832

GENERAL INFORMATION:

APPLICANT: AMITAGE, RICHARD
APPLICANT: DAVISON, BARRY
APPLICANT: FANSLAW, WILLIAM
APPLICANT: RENSRAW, BLAIR
APPLICANT: SPRIGGS, MELANIE
APPLICANT: WIDMER, MICHAEL
TITLE OF INVENTION: TREATMENT OF INDIVIDUALS EXHIBITING
TITLE OF INVENTION: DEFECTIVE CD40L (as amended)
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: word for windows 95, 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/589,771B
FILING DATE: January 22, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/009,258
FILING DATE: 01/22/93
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: HENRY, JANIS C.
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2810-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606

INFORMATION FOR SEQ ID NO:

8:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-589-771B-8

Query Match 44.6%; Score 1110; DB 3; Length 261;
Best Local Similarity 100.0%; Pred. No. 3.5e-79;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 257 HRLDKIEDERNLHEDVFVFKTTIORCNTGERSLSLNCSEIKSOEGFVKDMLNKEETK 316
Db 47 HRLDKIEDERNLHEDVFVFKTTIORCNTGERSLSLNCSEIKSOEGFVKDMLNKEETK 106
OY 317 KENEFEMKGDONPOIAAHVISEASSKTTISVLQMAEKGYTMSNNLVLENKQOLTVKRO 376
Db 107 KENEFEMKGDONPOIAAHVISEASSKTTISVLQMAEKGYTMSNNLVLENKQOLTVKRO 166

OY 377 GLYIYAQVTFPCSNREASSQAPFIASLCLKSPGFERILLRANANTHSSAKPCGOOSIHG 436
Db 167 GLYIYAQVTFPCSNREASSQAPFIASLCLKSPGFERILLRANANTHSSAKPCGOOSIHG 226
OY 437 GFVELQPGASVFVNVTDPQSVSHGTGFTSFGLLKL 471
Db 227 GFVELQPGASVFVNVTDPQSVSHGTGFTSFGLLKL 261

RESULT 13
PCT-US93-10034-4
Sequence 4, Application PC/TUS9310034
GENERAL INFORMATION:

APPLICANT: Spriggs, Melanie
APPLICANT: Stinivasan, Subhashini
TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10034
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia A
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 1003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO:

4:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-10034-4

Query Match 44.6%; Score 1110; DB 5; Length 261;
Best Local Similarity 100.0%; Pred. No. 3.5e-79;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 257 HRLDKIEDERNLHEDVFVFKTTIORCNTGERSLSLNCSEIKSOEGFVKDMLNKEETK 316
Db 47 HRLDKIEDERNLHEDVFVFKTTIORCNTGERSLSLNCSEIKSOEGFVKDMLNKEETK 106
OY 317 KENEFEMKGDONPOIAAHVISEASSKTTISVLQMAEKGYTMSNNLVLENKQOLTVKRO 376
Db 107 KENEFEMKGDONPOIAAHVISEASSKTTISVLQMAEKGYTMSNNLVLENKQOLTVKRO 166
OY 377 GLYIYAQVTFPCSNREASSQAPFIASLCLKSPGFERILLRANANTHSSAKPCGOOSIHG 436
Db 167 GLYIYAQVTFPCSNREASSQAPFIASLCLKSPGFERILLRANANTHSSAKPCGOOSIHG 226
OY 437 GFVELQPGASVFVNVTDPQSVSHGTGFTSFGLLKL 471
Db 227 GFVELQPGASVFVNVTDPQSVSHGTGFTSFGLLKL 261

RESULT 14

US-08-446-922-11
; Sequence 11, Application US/08446922
; Patent No. 5716805
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; APPLICANT: Srinivasan, Subhashini
; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,922
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/107,353
; FILING DATE: 08-13-93
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 1003-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-446-922-11

Query Match 44.0%; Score 1094.5; DB 1; Length 273;
Best Local Similarity 87.9%; Pred. No. 66-78; Mismatches 17; Indels 5; Gaps 2;
Matches 217; Conservative 8;
QY 226 LROQMEALKGKLRLEVAFSHOKAALPPDGR-RLDKTEDERNLHEDFVFMKTIOKNT 284
31 IEDKIEELSKYIHENIARIKLI---GERTSSDKIEDERNLHEDFVFMKTIOKNT 86
QY 285 GERSLSLNCIEIKSOFEGFKDMLNKEETKENSFEKQKDONQIAAHYISEASSKT 344
DB 87 GERSLSLNCIEIKSOFEGFKDMLNKEETKENSFEKQKDONQIAAHYISEASSKT 146
QY 345 TSVLOWAEKGYTWSNNLVLTLENGKQLTVKRGGLYIYAQVTFCSNREASSQAPFTASLC 404
DB 147 TSVLOWAEKGYTWSNNLVLTLENGKQLTVKRGGLYIYAQVTFCSNREASSQAPFTASLC 206
QY 405 LKSPGRERILLRAANHSSAKPCGOOSIHILGVFELQPGASVFVNVDPSVSHGTGFT 464
DB 207 LKSPGRERILLRAANHSSAKPCGOOSIHILGVFELQPGASVFVNVDPSVSHGTGFT 266
QY 465 SFGLLKL 471
DB 267 SFGLLKL 273

RESULT 15
US-08-249-189-21
; Sequence 21, Application US/08249189

Patent No. 5961974
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; TITLE OF INVENTION: NOVEL CYTOKINE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/249,189
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,703
; FILING DATE: October 23, 1992
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/805,723
; FILING DATE: December 5, 1991
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/783,707
; FILING DATE: October 25, 1991
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2802-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2065870430
; TELEFAX: 2065870606
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-249-189-21

Query Match 44.0%; Score 1094.5; DB 2; Length 273;
Best Local Similarity 87.9%; Pred. No. 66-78; Mismatches 17; Indels 5; Gaps 2;
Matches 217; Conservative 8;
QY 226 LROQMEALKGKLRLEVAFSHOKAALPPDGR-RLDKTEDERNLHEDFVFMKTIOKNT 284
31 IEDKIEELSKYIHENIARIKLI---GERTSSDKIEDERNLHEDFVFMKTIOKNT 86
QY 285 GERSLSLNCIEIKSOFEGFKDMLNKEETKENSFEKQKDONQIAAHYISEASSKT 344
DB 87 GERSLSLNCIEIKSOFEGFKDMLNKEETKENSFEKQKDONQIAAHYISEASSKT 146
QY 345 TSVLOWAEKGYTWSNNLVLTLENGKQLTVKRGGLYIYAQVTFCSNREASSQAPFTASLC 404
DB 147 TSVLOWAEKGYTWSNNLVLTLENGKQLTVKRGGLYIYAQVTFCSNREASSQAPFTASLC 206
QY 405 LKSPGRERILLRAANHSSAKPCGOOSIHILGVFELQPGASVFVNVDPSVSHGTGFT 464
DB 207 LKSPGRERILLRAANHSSAKPCGOOSIHILGVFELQPGASVFVNVDPSVSHGTGFT 266

Tue Jul 3 16:26:04 2001

us-09-454-223-2.ra1

Page 9

Oy 465 SFGLKL 471
| | | | |
Db 267 SFGLKL 273

Search completed: July 3, 2001, 16:15:31
Job time: 108 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2001, 16:14:03 ; Search time 20.96 seconds
(without alignments)
1711.747 Million cell updates/sec

Title: US-09-454-223-2
Perfect score: 2487

Sequence: 1 MLPFLSMVLVLPDGLGAEKMTLSORSYVNTCTLVWCSPTENGLPGHGRDGRGPRG 471

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: PIR,68:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1286	51.7	374	1 A42046	surfactant protein
2	1110	44.6	261	2 I53476	CD40 ligand - huma
3	1053	42.3	375	1 A45225	pulmonary surfacta
4	974	39.2	261	2 S53090	CD40 ligand - bovl
5	961.5	38.7	369	2 S33603	surfactant protein
6	879	35.3	371	2 I45678	conglutinin - bovl
7	878	35.3	371	1 JN0450	conglutinin precu
8	827	33.3	260	2 S21738	CD40 ligand - mous
9	565.5	22.7	301	2 A53570	collectin-43 - bov
10	488.5	19.6	888	2 S28791	collagen alpha 1(X
11	484.5	19.5	1049	1 CG807S	collagen alpha 1(I
12	481	19.3	1042	1 CG81S	collagen alpha 1(I
13	480	19.3	1806	1 CG81E	collagen alpha 1(X
14	479.5	19.3	1838	1 CG81V	collagen alpha 1(X
15	479.5	19.3	1843	2 S18803	collagen alpha 1(V
16	477.5	19.2	1464	2 S59856	collagen alpha 1(I
17	477	19.2	671	1 CG81S	collagen alpha 1(I
18	476.5	19.2	1453	2 S21626	collagen alpha 1(I
19	476	19.1	1532	2 A61262	collagen alpha 1(X
20	475	19.1	1433	2 A46053	bullous pemphigoid
21	474.5	19.1	1464	1 CG81S	collagen alpha 1(I
22	474.5	19.1	1466	1 CG81V	collagen alpha 1(I
23	473.5	19.0	1487	1 CG81E	collagen alpha 1(I
24	473.5	19.0	1487	1 CG81E	collagen alpha 1(X
25	473	19.0	1492	2 A40333	collagen alpha 1(I
26	472.5	19.0	779	1 CG81S	collagen alpha 1(I
27	472.5	19.0	1763	1 S16366	collagen alpha 1(I
28	472	19.0	1418	2 T45467	collagen alpha 1(I
29	471	18.9	1486	1 B40333	collagen alpha 1(I

30	470.5	18.9	1024	2 S18251	collagen alpha 1(X
31	470	18.9	918	2 S23377	collagen alpha 2(V
32	470	18.9	1022	2 S04111	collagen alpha 2(V
33	469.5	18.9	1419	2 A41182	collagen alpha 1(I
34	469.5	18.9	1487	2 B41182	collagen alpha 1(I
35	469.5	18.9	2944	2 A54649	collagen alpha 1(I
36	469	18.9	886	2 I50694	collagen alpha 1(I
37	468.5	18.8	482	2 B31795	collagen alpha 1(X
38	467.5	18.8	1142	2 JX0369	collagen alpha 1(X
39	465.5	18.7	1497	2 I49607	procollagen type V
40	465.5	18.7	1549	2 I48103	type VII collagen
41	465	18.7	730	2 A36226	collagen alpha 1 c
42	464	18.7	1146	2 A38587	collagen, cornea-8
43	463.5	18.6	1414	1 S23809	collagen alpha 2(I
44	462.5	18.6	1496	1 CG81V	collagen alpha 2(V
45	461.5	18.6	680	2 S31216	collagen alpha 1(X

ALIGNMENTS

RESULT 1
A42046
surfactant protein D - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text, change 10-Sep-1999
C:Accession: A42046
R:Shimizu, H.; Fisher, J.H.; Papst, P.; Benson, B.; Lau, K.; Mason, R.J.; Voelker, D.
J. Biol. Chem. 267, 1853-1857, 1992
A:Title: Primary structure of rat pulmonary surfactant protein D: C-type lectin homology
A:Reference number: A42046; M0ID:92112913
A:Accession: A42046
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <SH1>
A:Cross-references: GB:M81231; NID:g207035; PION:AAA42170.1; PID:g207036
A:Experimental source: Lung
A>Note: Sequence extracted from NCBI backbone (NCBI:76027, NCBI:76031)
C:Superfamily: pulmonary surfactant protein D: C-type lectin homology
F:253-372/Domain: C-type lectin homology <LCH>

Query Match 51.7%; Score 1286; DB 1; Length 374;
Best Local Similarity 85.7%; Pred. No. 1.5e-72;
Matches 245; Conservative 7; Mismatches 34; Indels 0; Gaps 0;
QY 1 MLPFLSMVLVLPDGLGAEKMTLSORSYVNTCTLVWCSPTENGLPGHGRDGRGPRG 60
DB 1 MLPFLSMVLVLPDGLGAEKMTLSORSYVNTCTLVWCSPTENGLPGHGRDGRGPRG 60
QY 61 EKGDDGLPSPMGLSGDQPTGPGVPGKENGSGAGEPGKRGSGPPGLPIPGAPGKG 120
DB 61 EKGDDGLPSPMGLSGDQPTGPGVPGKENGSGAGEPGKRGSGPPGLPIPGAPGKG 120
QY 121 PSKGONIGPGKPGKGEAPGKGEVAPGKMGSTGKSGTGPKGRCAPGVGAGGNG 180
DB 121 PSKGONIGPGKPGKGEAPGKGEVAPGKMGSTGKSGTGPKGRCAPGVGAGGNG 180
QY 181 AAGPACPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPG 240
DB 181 AAGPACPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAP 240
QY 241 EAFPSHYOKAALFPPDGHRRDLKTEDENLHDFVFMKTIQRCNTGE 286
DB 241 EAFPSHYOKAALFPPDGHRRDLKTEDENLHDFVFMKTIQRCNTGE 286
RESULT 2
153476
CD40 ligand - human
N:Alternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP protol
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence, revision 02-Jul-1996 #text, change 08-Oct-1999

C:Accession: I53476; S28017; JH0793; S26694; S28852; S25684; S30593
R:Gauchat, J.
FEBS Lett. 315, 259-266, 1992
A:Title: Human CD40-1192: Molecular cloning, cellular distribution and regulation of
A:Reference number: I53476; MUID:93138085
A:Accession: I53476
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-261 <RES>
A:Cross-references: GB:U07414; NID:9180123; PIDN:AAA35662.1; PID:9180124
R:Hollenbaugh, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny, N.J.; Bresch-Andersen, S.;
EMBO J. 11, 4313-4321, 1992
A:Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand for
A:Reference number: S28017; MUID:93049181
A:Accession: S28017
A:Molecule type: mRNA
A:Residues: 1-261 <HOL>
A:Cross-references: EMBL:215017; NID:938483; PIDN:CAA78737.1; PID:938484
R:Spriggs, M.K.; Armitage, R.J.; Strohman, L.; Clifford, K.N.; Macduff, B.M.; Sato, T.
J. Exp. Med. 176, 1543-1550, 1992
A:Title: Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobulin
A:Reference number: JH0793; MUID:93094757
A:Accession: JH0793
A:Molecule type: mRNA
A:Residues: 1-261 <SPR>
A:Cross-references: GB:X67878; NID:938411; PIDN:CAA48077.1; PID:938412
R:Graf, D.; Korthaus, U.; Mages, H.W.; Senger, G.; Krocsek, R.A.
Eur. J. Immunol. 22, 3191-3194, 1992
A:Title: Cloning of TRAP, a ligand for CD40 on human T cells.
A:Reference number: S26694; MUID:93076854
A:Accession: S26694
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-261 <GRA>
A:Cross-references: EMBL:X68550; NID:937269; PIDN:CAA48554.1; PID:937270
R:Gauchat, J.F.; Aubry, J.P.; Mazzei, G.; Lile, P.; Tomotte, T.; Elson, G.; Bonnefoy, J.
FEBS Lett. 315, 259-266, 1993
A:Title: Human CD40-ligand: molecular cloning, cellular distribution and regulation of
A:Reference number: S28852; MUID:93138085
A:Accession: S28852
A:Molecule type: mRNA
A:Residues: 1-261 <GRA>
A:Cross-references: EMBL:U07414; NID:9180123; PIDN:AAA35662.1; PID:9180124
A:Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 6-Gln
C:Genetics:
A:Gene: GDB:CD40LG; HIGM1; IMD3
A:Cross-references: GDB:120632; OMIM:308230
A:Map position: Xq26-q26
A:Keywords: glycoprotein; transmembrane protein
A:3-44/Domain: transmembrane #status predicted <TM>
A:45-261/Domain: extracellular #status predicted <EXT>
F:6,240/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 44.6%; Score 1110; DB 2; Length 261;
Best Local Similarity 100.0%; Pred. No. 7.4e-62;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

257 HRLDKLDEDEBNLHEDFVFMKTICRCNTGERSLSLNCCEIKSQEGFVKDILNKEETK 316
DB HRLDKLDEDEBNLHEDFVFMKTICRCNTGERSLSLNCCEIKSQEGFVKDILNKEETK 106
317 KINSFEMQKDONPOIAHAYSEASSKTSYLVQMAEKGYTMMNLVTLNKGKQLTVKRO 376
DB KINSFEMQKDONPOIAHAYSEASSKTSYLVQMAEKGYTMMNLVTLNKGKQLTVKRO 166
377 GLYYIAOVYFCNSREASAPFASICLKSPGREPRLILRAANHSSAKKPGCGOSIHLC 436
DB GLYYIAOVYFCNSREASAPFASICLKSPGREPRLILRAANHSSAKKPGCGOSIHLC 226
437 GFELQPGASVFVNVDPSQVSHGTFSTGLKL 471
GFELQPGASVFVNVDPSQVSHGTFSTGLKL 471

DB 227 GFELQPGASVFVNVDPSQVSHGTFSTGLKL 261

RESULT 3
A45225
pulmonary surfactant protein D precursor - human
N:Alternate names: SP-D
C:Date: 16-Apr-1999 #sequence revision 16-Apr-1999 #text change 22-Jun-1999
C:Accession: A45225; S23434; S24555; S44420; S18382; A56776
R:Crouch, E.; Rust, K.; Velle, R.; Donis-Keller, H.; Grosso, L.
J. Biol. Chem. 268, 2976-2983, 1993
A:Title: Genomic organization of human surfactant protein D (SP-D). SP-D is encoded o
A:Reference number: A45225; MUID:93155122
A:Accession: A45225
A:Molecule type: DNA
A:Residues: 1-375 <CRO>
A:Cross-references: GB:L05483; GB:L05484; GB:L05485; NID:9292505; PIDN:AAB59450.1; PI
A:Experimental source: placenta
A:Note: sequence extracted from NCBI backbone (NCBI:124316)
R:Lu, J.; Mills, A.C.; Reid, K.B.M.
Biochem. J. 284, 795-802, 1992
A:Title: Purification, characterization and cDNA cloning of human lung surfactant pro
A:Reference number: S23434; MUID:92322003
A:Accession: S23434
A:Molecule type: mRNA
A:Residues: 1-30, 'T', '32-121, 'P', '123-179, 'A', '181-375 <LNU1>
A:Cross-references: EMBL:X65018; NID:934766; PIDN:CAA46152.1; PID:934767
A:Experimental source: lung
A:Accession: S24555
A:Molecule type: protein
A:Residues: 214-234, 'X', '236, 'XX', '239-241 <LNU2>
R:Hoppe, H.J.; Barlow, P.N.; Reid, K.B.M.
FEBS Lett. 344, 191-195, 1994
A:Title: A parallel three stranded alpha-helical bundle at the nucleation site of col
A:Reference number: S44420; MUID:94244769
A:Accession: S44420
A:Molecule type: mRNA
A:Residues: 202-257 <HOP>
R:Rust, K.; Grosso, L.; Zhang, V.; Chang, D.; Persson, A.; Longmore, W.; Cal, G.L.; C
Arch. Biochem. Biophys. 290, 116-126, 1991
A:Title: Human surfactant protein D: SP-D contains a C-type lectin carbohydrate recog
A:Reference number: S18382; MUID:91378578
A:Accession: S18382
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 'F', '60-205, 'P', '207-374, 'HF' <RUS>
A:Cross-references: GB:L05485; NID:9292505
A:Note: corrections to this sequence are reported in reference A56776
R:Crouch, E.; Persson, A.; Chang, D.
Am. J. Pathol. 142, 241-248, 1993
A:Title: Accumulation of surfactant protein D in human pulmonary alveolar proteinosis
A:Reference number: A56776; MUID:93142849
A:Accession: A56776
A:Status: preliminary
A:Molecule type: protein
A:Residues: 46-58, 'F', '60-62, 'E', '64-72, '223-227, 'X', '229-239, 'P', '241-245, 'X', '247-256, 'X'
A:Cross-references: PIDN:AAB5037.1; PID:9263973; PIDN:AAB25038.1; PID:9263974
A:Experimental source: bronchoalveolar lavage
A:Note: Sequence extracted from NCBI backbone (NCBI:123024, NCBI:123023); sequence
C:Comment: Pulmonary surfactant is a complex of phospholipids and proteins that lower
C:Genetics:
A:Gene: GDB:SFPPD; SFTPD; SP-D
A:Cross-references: GDB:132674; OMIM:178635
A:Map position: 10q22.2-10q23.1
C:Superfamily: pulmonary surfactant protein D: C-type lectin homology
C:Keywords: blocked amino end; calcium; glycoprotein; hydroxylsine; hydroxyproline;
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-375/Product: pulmonary surfactant protein D #status predicted <MAT>
F:21-45/Domain: non-collagenous #status predicted <NC1>
F:46-222/Domain: collagenous #status predicted <COL>
F:223-375/Domain: non-collagenous #status predicted <NC2>

F:254-373/Domain: C-type lectin homology <LCH>
F:90/Binding site: carbohydrate (Asn) #status predicted
F:281-373,351-365/Disulfide bonds: #status predicted

Query Match	42.3%	Score 1053	DB 1	Length 375
Best Local Similarity	72.6%	Pred 0.38e-58		
Matches 191	Conservative 28	Mismatches 44	Indels 0	Gaps 0

OY	1	MPLFSLMVLVLPOLNLCNEMSLQSRSVPTNTCLVMCSPTENGCLPDRDRDRGREGRG	60
OY	2	LFLFLSLVLLVLTQPLGLYLEAKMTYSHRTMPASCTLVMCSSVEEGSLPDRDRDRGREGRG	61
OY	61	ENGCDGLPCPCKMLSTGLQCPGPVYPKGKENGCSAGEPCKGKENGSLSGPPEGLPCTPGCPAGKEG	120
OY	62	EGKGDPLPCMAAGCAGAPGQAGPVGPKDNDSSVCGPFGKGDTPGPGPGPPGPPVCPAGREG	121
OY	121	PGCKGGINPGCKPGPKGKEGAPKGEVCAFPKMGOSTGAKGSGTGPCKGERAPVVOGAPGKAG	180
OY	122	ALCKGKGINPGCKPGPKGKEGAPKGEVCAFPKMGOSAGARGLAGPPGCKERYPDERGVPGATG	181
OY	181	AAGPAGPAGPQAGPAGSRGPPGLKGDRCVPQDGRGIGKSGSLPDSALRQOMEALKGLQRL	240
OY	182	AAGSGAGAMPQGSPPGARGPGLTGDKDIPGDKAGKSGSLPDSVASTLRQOVALGGOVYHL	241
OY	241	EVAFSHYKAAALFPPDGHRLDKI 263	
OY	242	QAFFSQYKVELFPPNGOSVGEKI 264	

RESULT 4
S53090
CD40 Ligand - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
C:Accession: S53090
R:Merits, B.E.L.C.: Murliuk, M.
submitted to the EMBL Data Library, February 1995
A:Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB
A:Reference number: S53090
A:Accession: S53090
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-261 <MER>
A:Cross-references: EMBL:Z4B469; NID:g732569; PIDN:CAA88363.1; PID:g732570

Query Match	39.2%	Score 974	DB 2	Length 261
Beat Local Similarity	88.4%	Pred. No. 1.9e-53		
Matches 190	Conservative	5	Mismatches 20	Indels 0
			Gaps	0
QY	257	HRRLDKIEDERNLHEDFVFMKTIQRNCNTERGSRSLNLNCEEIKSQEGEFVKDMLNKEETK	316	
DB	47	HRRLDKIEDERNLHEDFVFMKTIQRNCNCEGSLNLNCEEIRSFEDLVKDIMQKEVKK	106	
QY	317	KERSFEMQKQDNOQIAHVITSEASSKTTSVLQMAKGYTMSNLYLLENGKOLTVRQ	376	
DB	107	KERNFEMHKGGQEPQIAHVITSEASSKTTSVLQMAKGYTTLNNLYLLENGKOLTAVRQ	166	
QY	377	GLYIYIAQVTFPCSNRREASSQAFITSLCLSPCFERFILLRPAANTHSSAKPCGQOSIHG	436	
DB	167	GFYIYIYQVTFPCSNRRETLQAFITSLCLSPGSEERILLRPAANTHSSAKPCGQOSIHG	226	
QY	437	GVFELDPCGASVFNVTQPSOVSHGTFGLLKL	471	
DB	227	GVFELDGSASVFNVTQPSOVSHGTFGLLKL	261	

RESULT 5
S33603
surfactant protein D - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999

C:Accession: S33603
R:Lim, B.L.; Lu, J.; Reid, K.B.M.
Immunology 76, 159-165, 1993
A>Title: Structural similarity between bovine conglutinin and bovine lung surfactant
A:Reference number: S33603; MUID:93170856
A:Accession: S33603
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-369 <LIM>
C:Superfamily: pulmonary surfactant protein D; C-type lectin homology
F:248-367/Domain: C-type lectin homology <LCH>

Query Match	38.7%	Score	961.5;	DB	2;	Length	369;
Best Local Similarity	56.6%	Pred	NO	1.7e-52;			
Matches	192;	Conservative	43;	Mismatches	75;	Indels	29;
						Gaps	6

```

0Y 1 MBPFLMVLVLYOPPLGMLGEMKSLSONSVNTCTLVNCSPLNGNIPGMDGRGREGPRG 60
0Y 2 LRP-LSTVLLLTJTPQWMSLGAEMKTYSQTMANNACTLVNCSPPEDGLPGMDGRGREGPRG 61
0Y 3 LRP-LSTVLLLTJTPQWMSLGAEMKTYSQTMANNACTLVNCSPPEDGLPGMDGRGREGPRG 61
0Y 61 EKGDPLPGMBGLSGLOGPTCPVPGKGENSGAGEBPGRKGLSGPPGLPIPGPAGKEG 120
0Y 62 EKGDPPSPGPAGNAGMPPGAPPIGLTKGNGSAGEBPGRGD---TGPPGPMPGPGAGREG 118
0Y 121 PSKGNGNIGPOGRKPRPGEGAPKCEVGAPEGMGSTGANGSTGPKCEBGAPEVOGAPGMAG 180
0Y 119 PSKGOSMGPPGPPIPGPGDGTGPKGCVGAPIGQS---PGAPLKEBGRGAPGDGAPGRAG 175
0Y 181 AAGPAGPAGQOGAPGSGSPPELKKDRCYVGDRTIGESGLPDSALROOMEALKGLORL 240
0Y 176 APBPRGAIIGOGSGGAPGPELKKDRCYVGDRTIGESGLPDSALROOMEALKGLORL 235
0Y 241 EVAFSHYOKAALPPDGHRRLDKIDERRLHDFVAMKTIORCNTG-----ERS 288
0Y 236 ONAFSOTKRMALPPNGRSVGEKI--FKVVGSEKTFODAOOITVOAGGOLPSPRGAENEA 293
0Y 289 LSLNLCEEIKSOFEGFVKDILNKEETKKESEFMOKG 327
0Y 294 LTOLATAONKAALF-----LSMSDTRKEGFTIPTGE 324

```

RESULT **6**

145878
conglutinin - bovine
C.Species: Bos primigenius taurus (cattle)
C.Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 20-Aug-1999
C.Accession: I45878
R.Liou, L.S.; Sasstry, R.; Hartshorn, K.L.; Lee, Y.M.; Okarma, T.B.; Tauber, A.I.; Sasstry,
Gene 141, 277-281, 1994
A.Title: Bovine conglutinin (BC) mRNA expressed in liver: cloning and characterization
A.Reference number: I45878; M0ID:94215917
A.Accession: I45878
A.Status: preliminary;
A.Molecule type: mRNA
A.Residues: 1-371 <L1O>
A.Cross-references: GB:I48871, NID:g495012, PIDN:AAA0126.1, PID:g495013
C.Superfamily: pulmonary surfactant protein D, C-type lectin homology
F:248-369/Domcln: C-type lectin homology <LCHe>

Query Match	35.3%	Score 879	DB 2	Length 371	
Best Local Similarity	49.5%	Pred. No. 2.1e+47			
Matches 180	Conservative 45	Mismatches 87	Indels 52	Gaps 6	
QY	1	MLPLSMVLVLP	LGNGIAEKKSL	SORSVPNTCTLVMCSPTENG	LPGRDGRREGPRG 60
	:		:	:	
	:		:	:	
DB	3	LPL-LSVLLLT	TOPPRSRGA	ENTTFSSQKLIANACTLVMCSPL	LBGLPQHDDQDGR
	:	:	:	:	
	:	:	:	:	
QY	61	EKGDPGLPG	PMGLSLQGP	EVYGPKEGNSA	PEPCKGERSGLSGPGLPGIPG
	:	:	:	:	
	:	:	:	:	
DB	62	EKGDPSPG	PPGRGRGR	PPQWGP	IGKPGDNGFVYGE
	:	:	:	:	
	:	:	:	:	

mur. J. Biochem. 215, 793-799, 1993

361 NLVT 364

C:Superfamily:pulmonary surfactant protein D; C-type lectin homology
C:Keywords:lectin
F:177-299/Domain: C-type lectin homology <LCH>

Query Match 22.7%; Score 565.5; DB 2; Length 301;
Best Local Similarity 35.8%; Pred. No. 4.1e-28;
Matches 127; Conservative 42; Mismatches 81; Indels 105; Gaps 8;

OY 21 EKSLRSRVNTCTLVMSPTENGLPGRDGRDREGPRGEGDPGLPGMGLSGLQPT 80
|||:::||||:::|||||
DB 2 EMGVYSKRTLDPCLVLCAPPADSLRGHDGRDEKGCPGEGDP----- 46

OY 81 GPVGPCKEENGASAGECPKGERGLSGPPCLPGIPAGKEGPSGKOCNIGCPGPKGEA 140
|||:::||||:::|||||
DB 47 -----GPPGM---PQPAGREGPSGROGSMCGPFGPKCEP 79

OY 141 GPKGVECAPMGOSTGAKGSTGKERGARPCVGACAPNAGAAGPAGPQGAPGSRPP 200
|||:::||||:::|||||
DB 80 GPGGGVAPAGMPGS---PQPAGLGKRGAP-----GPGCAIGPQGGSGAMGP 124

OY 201 GLKGDRCVPVCGRGICGESGLPDSSALRQOMEGALKGLRLYEAFSHYOKALPFDRHRL 260
|||||:::||||:::|||||
DB 125 GLKGDRCDDPGKGAGETSVLEVDTLRORMRNLEGEVORLNIVTYRKAVLPDGQAVG 184

OY 261 DKIEDERNLHEDFYEMKTIRQCNTGERSLSLNCSEIKSQF-----EGF 304
::|
DB 185 EKI-----FKTAGAVKSYSDAEOL-----CREAKQLASPSSAEAEAVTQLVRAK 230

OY 305 VKDIMLNKEETKKENSFEQKQ-----DONPOIAAHYISEAS 341
|||:::||||:::|||||
DB 231 NKHAAYLSMNDSKEKGFYPTGSSLDYSNMAPEGNPNRAKDSDPENCLERYSDON 285

RESULT 10
528791
collagen alpha 1(XI) chain - chicken (fragment)
C:Species: Gallus gallus (chicken)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
C:Accession: S28791
J:Nah, H.D.; Barembaum, M.; Upholt, W.B.
R:Biol. Chem. 267, 22581-22586, 1992
A>Title: The chicken alpha1(XI) collagen gene is widely expressed in embryonic tissue
A:Reference number: 528791; MUID:93054557
A:Accession: S28791
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-888 <NAH>
A:Cross-references: EMBL:M88593; NID:g211619; PIDN:AAA48707.1; PID:g211620
C:Superfamily: collagen alpha 1(V) chain; fibrillar collagen carboxyl-terminal homo
F:665-887/Domain: fibrillar collagen carboxyl-terminal homology <FC>

Query Match 19.6%; Score 488.5; DB 2; Length 888;
Best Local Similarity 47.7%; Pred. No. 8.3e-23;
Matches 102; Conservative 17; Mismatches 62; Indels 33; Gaps 4;

OY 41 PTENGLPGRDGRDREGPRGEGDPGLPGMGLSGLQPTGPVGP-----GE 88
|||:::||||:::|||||
DB 399 GPPGCEGPCAGODGVGGEKEDGDDPGOPGPPGSCGEACPPGPKRCPCATGACAGERGE 458

OY 89 NGSAEP-----GPKGERGLSGPPGLPGIPAGKE-----GPSGKOGNIGP 130
|||:::||||:::|||||
DB 459 KGAKGEGFACGACTGTGPPGQPGACRPGELGRICPVGVGEGGLPCGAPCODGPGCHLGP 518

OY 131 OGKPPGPGGEAPKPGVGARCMOGSTGAKGSTGKERGARPCVGACAPNAGAAGPAGP 187
|||:::||||:::|||||
DB 519 PGLGLGLDPPSKGKHGHLGLIGPPGEDGEGDKGLPGQSGPAKADKDISGPAGP 578

OY 188 AGPQAGCSRPPLGLKGDRCVPGDRGIKESGLP 221
|||:::||||:::|||||
DB 579 LGPPGPPGLPFPQGPKGSGSSGPAGQKCDISGLP 612

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2001, 16:15:03 ; Search time 12.03 Seconds
(without alignments)
1341.175 Million cell updates/sec

Title: US-09-454-223-2

Perfect score: 2487
Sequence: 1 MLPRLSMVLVQLVQPLGNLGA.....TDPQGVSHGTGTFSGILLKL 471

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1384.5	55.7	374	1	PSPD_MOUSE
2	1286	51.7	374	1	PSPD_RAT
3	1110	44.6	261	1	TNFS_HUMAN
4	1053	42.3	375	1	PSPD_HUMAN
5	974	39.2	261	1	TNFS_BOVIN
6	967.5	38.9	369	1	PSPD_BOVIN
7	939.5	37.8	260	1	TNFS_FELCA
8	907.5	36.5	260	1	TNFS_CANFA
9	878	35.3	371	1	CONC_BOVIN
10	827	33.3	260	1	TNFS_MOUSE
11	565.5	22.7	301	1	CLA3_BOVIN
12	484.5	19.5	1049	1	CLA3_BOVIN
13	482.5	19.4	1460	1	CLA3_BOVIN
14	481.5	19.4	1463	1	CLA3_BOVIN
15	481	19.3	1454	1	CLA3_BOVIN
16	480.5	19.3	1804	1	CLA3_BOVIN
17	480	19.3	1806	1	CLA3_BOVIN
18	478	19.2	1650	1	CLA3_BOVIN
19	477.5	19.2	1464	1	CLA3_BOVIN
20	476.5	19.2	1453	1	CLA3_BOVIN
21	476.5	19.2	1838	1	CLA3_BOVIN
22	475	19.1	1466	1	CLA3_BOVIN
23	474.5	19.1	1466	1	CLA3_BOVIN
24	474	19.1	1736	1	CLA3_BOVIN
25	473.5	19.0	1418	1	CLA3_BOVIN
26	472.5	19.0	1418	1	CLA3_BOVIN
27	472.5	19.0	1763	1	CLA3_BOVIN
28	470.5	18.9	911	1	CLA3_BOVIN
29	470	18.9	1022	1	CLA3_BOVIN
30	469.5	18.9	1459	1	CLA3_BOVIN
31	469.5	18.9	2944	1	CLA3_BOVIN
32	468.5	18.8	482	1	CLA3_BOVIN
33	462.5	18.6	747	1	CLA3_BOVIN

34	462.5	18.6	1364	1	CA21_BOVIN	P02465 bos taurus
35	462.5	18.6	1496	1	CA21_HUMAN	P03597 homo sapien
36	461.5	18.6	630	1	CA1A_MOUSE	O05306 mus musculu
37	461	18.5	635	1	CA2A_HUMAN	P25067 homo sapien
38	460.5	18.5	1685	1	CA5A_HUMAN	P29400 homo sapien
39	458.5	18.4	1366	1	CA21_CANFA	O46392 canis famli
40	458.5	18.4	1373	1	CA21_MOUSE	O01149 mus musculu
41	457.5	18.4	1362	1	CA21_CHICK	P02467 gallus gall
42	456.5	18.4	1027	1	CA21_RIPPA	P30754 rippa pach
43	456	18.3	744	1	CA1B_RABIT	P14282 oryctolagus
44	456	18.3	921	1	CA1D_MOUSE	O05722 mus musculu
45	455	18.3	754	1	CA5A_CANFA	O28247 canis famli

ALIGNMENTS

RESULT ID	SPSD_MOUSE	STANDARD	PRT	374 AA.
AC	P50404:			
DT	01-OCT-1996 (rel. 34, Created)			
DT	01-OCT-1996 (rel. 34, Last sequence update)			
DT	15-JUL-1999 (rel. 38, Last annotation update)			
DE	PULMONARY SURFACTANT-ASSOCIATED PROTEIN D PRECURSOR (SP-D) (PSP-D).			
GN	SFTPD OR SFTPA.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
ON	NCBI_TaxID=10090;			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-B6/CBA; TISSUE=Lung;			
RX	MEDLINE=96094460; PubMed=7499852;			
RA	Motwani M., White R.A., Guo N., Dowler L.L., Tauber A.I., Sasstry K.N.,			
RT	Mouse surfactant protein-D. cDNA cloning, characterization, and gene			
RT	localization to chromosome 14.*			
RL	J. Immunol. 155:5671-5677(1995).			
CC	- FUNCTION: CONTRIBUTES TO THE LUNG'S DEFENSE AGAINST INHALED			
CC	MICROORGANISMS. BINDS STRONGLY MALTOSE RESIDUES AND TO A LESSER			
CC	EXTENT OTHER ALPHA-GLUCOSYL MOETIES. IT COULD PARTICIPATE IN THE			
CC	EXTRACELLULAR REORGANIZATION OR TURNOVER OF PULMONARY SURFACTANT.			
CC	- SUBUNIT: OLIGOMERIC COMPLEX OF 4 SET OF HOMOTRIMERS.			
CC	- SUBCELLULAR LOCATION: EXTRACELLULAR.			
CC	- MISCELLANEOUS: PULMONARY SURFACTANT CONSISTS OF 90% LIPID AND 10%			
CC	PROTEIN. THERE ARE 4 SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGENOUS,			
CC	CARBOHYDRATE-BINDING GLYCOPROTEINS (SP-A AND SP-D) AND 2 SMALL			
CC	HYDROPHOBIC PROTEINS (SP-B AND SP-C).			
CC	- SIMILARITY: CONTAINS A COLLAGENOUS DOMAIN.			
CC	- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.			
CC	- This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
DR	EMBL: L40156; AAA92021.1; ..			
DR	HSSP: P19999; IMB.			
DR	MGI: 109515; Sftpd.			
DR	InterPro: IPR000087; ..			
DR	InterPro: IPR001304; ..			
DR	Pfam: PF01391; Collagen; 3.			
DR	Pfam: PF00059; Lactin; 1.			
DR	PROSITE: PS00615; C-TYPE LECTIN_1; 1.			
DR	PROSITE: PS00641; C-TYPE LECTIN_2; 1.			
KW	Glycoprotein; Calcium; Surface film; Gaseous exchange; Hydroxylation;			
FT	Signal; Lactin; Collagen; Repeat; Coll coll.			
FT	SIGNAL 1 19			
FT	CHAIN 20 374			
FT	D.			

FT DOMAIN 45 221 COLLAGEN-LIKE.
 FT DOMAIN 222 253 COILED COIL (POTENTIAL).
 FT DISULFID 278 374 C-TYPE LECTIN (SHORT FORM).
 FT DISULFID 280 372 BY SIMILARITY.
 FT CARBOHYD 350 364 BY SIMILARITY.
 FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 374 AA: 37688 MW: FE034261263F43E4 CRC64;

Query Match 55.7%; Score 1384.5; DB 1; Length 374;
 Best Local Similarity 95.3%; Pred. No. 3.1e-70;
 Matches 262; Conservative 0; Mismatches 10; Indels 3; Gaps 1;

QY 1 MLPLSLMLVLYVOPICNLGAEMKSLQSRSVPNTCTLYMCSPTENGILPGRDGRDREGPRG 60
 DB 1 MLPLSLMLVLYVOPICNLGAEMKSLQSRSVPNTCTLYMCSPTENGILPGRDGRDREGPRG 60
 QY 61 EKGDPLGPGMGLSLGQPTGPGVPGKENGSGEPKRGSLSGPGLGIPGPAKREG 120
 DB 61 EKGDPLGPGMGLSLGQPTGPGVPGKENGSGEPKRGSLSGPGLGIPGPAKREG 120
 QY 121 PSKGQNGTGPCKPKKEAGPKGEVGAAGMGSTGAKSGTGPKEGAPGVGAGAGNAG 180
 DB 121 PSKGQNGTGPCKPKKEAGPKGEVGAAGMGSTGAKSGTGPKEGAPGVGAGAGNAG 180
 QY 181 AAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAG 240
 DB 181 AAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAG 240
 QY 241 EVAFSHQKALPPDGHRRLDKI--EDERNLHED 272
 DB 241 EVAFSHQKALPPDGHRRLDKI--EDERNLHED 272
 QY 241 EVAFSHQKALPPDGHRRLDKI--EDERNLHED 272
 DB 241 EVAFSHQKALPPDGHRRLDKI--EDERNLHED 272
 RESULT 2
 PSTD_RAT STANDARD; PRT; 374 AA.
 ID PSTD_RAT
 AC P35348;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PULMONARY SURFACTANT-ASSOCIATED PROTEIN D PRECURSOR (SP-D) (PSP-D)
 GN SPSPD OR SPSP4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 20-33.
 RA TISSUE=Lung;
 RA MEDLINE=92112913; PubMed=1370483;
 RA Shlimiz H., Fisher J.H., Papst P., Benson B., Lau K., Mason R.J.,
 Voelker D.R.;
 RA "Primary structure of rat pulmonary surfactant protein D. cDNA and
 deduced amino acid sequence.";
 RA J. Biol. Chem. 267:1853-1857(1992).
 RL [2]
 RP SEQUENCE OF 73-95 AND 153-180.
 RC TISSUE=Lung;
 RA MEDLINE=90001186; PubMed=2675969;
 RA Person A., Chang D., Rust K., Moxley M., Longmore W., Crouch E.;
 RA "Purification and biochemical characterization of CP4 (SP-D), a
 collagenous surfactant-associated protein.";
 RA Biochemistry 28:6361-6367(1989).
 RL [1]
 RP FUNCTION: CONTRIBUTES TO THE LUNG'S DEFENSE AGAINST INHALED
 MICROORGANISMS. BINDS STRONGLY MALTOSE RESIDUES AND TO A LESSER
 EXTENT OTHER ALPHA-GLUCOSYL MOIETIES. IT COULD PARTICIPATE IN THE
 EXTRACELLULAR REORGANIZATION OF TURNOVER OF PULMONARY SURFACTANT.
 CC SUBUNIT: OLIGOMERIC COMPLEX OF 4 SET OF HOMOTRIMERS.
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- MISCELLANEOUS: PULMONARY SURFACTANT CONSISTS OF 90% LIPID AND 10%
 PROTEIN. THERE ARE 4 SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGENOUS,

CC CARBOHYDRATE-BINDING GLYCOPROTEINS (SP-A AND SP-D) AND 2 SMALL
 CC HYDROPHOBIC PROTEINS (SP-B AND SP-C).
 CC -1- SIMILARITY: CONTAINS A COLLAGENOUS DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC EMBL: M81231; AAA42170.1; -
 CC PIR: A42046; A42046.
 CC HSSP: P19999; JMSB.
 CC InterPro: IPR000087; -
 CC InterPro: IPR001304; -
 CC Pfam: PF00059; Lectin.C; 1.
 CC PROSITE: PS00615; C-TYPE LECTIN_1; 1.
 CC PROSITE: PS50041; C-TYPE LECTIN_2; 1.
 CC GlycoProfile: Calcium; Surface film; Gaseous exchange; Hydroxylation;
 CC Signal; Lectin; Collagen; Repeat; Coiled coil.
 CC SIGNAL 1
 CC CHAIN 20 374
 CC FT 20 374
 CC FT DOMAIN 45 221
 CC FT DOMAIN 222 253
 CC FT DISULFID 278 374
 CC FT DISULFID 280 372
 CC FT DISULFID 350 364
 CC FT CARBOHYD 89 89
 CC FT MOD_RES 77 77
 CC FT MOD_RES 86 86
 CC FT MOD_RES 95 95
 CC FT MOD_RES 98 98
 CC FT MOD_RES 170 170
 CC FT MOD_RES 176 176
 CC FT CONFLICT 89 89
 CC FT CONFLICT 164 164
 CC SQ SEQUENCE 374 AA: 37561 MW: DB2B5E39DB4A3C CRC64;

Query Match 51.7%; Score 1286; DB 1; Length 374;
 Best Local Similarity 85.7%; Pred. No. 8.8e-65;
 Matches 245; Conservative 7; Mismatches 34; Indels 0; Gaps 0;

QY 1 MLPLSLMLVLYVOPICNLGAEMKSLQSRSVPNTCTLYMCSPTENGILPGRDGRDREGPRG 60
 DB 1 MLPLSLMLVLYVOPICNLGAEMKSLQSRSVPNTCTLYMCSPTENGILPGRDGRDREGPRG 60
 QY 61 EKGDPLGPGMGLSLGQPTGPGVPGKENGSGEPKRGSLSGPGLGIPGPAKREG 120
 DB 61 EKGDPLGPGMGLSLGQPTGPGVPGKENGSGEPKRGSLSGPGLGIPGPAKREG 120
 QY 121 PSKGQNGTGPCKPKKEAGPKGEVGAAGMGSTGAKSGTGPKEGAPGVGAGAGNAG 180
 DB 121 PSKGQNGTGPCKPKKEAGPKGEVGAAGMGSTGAKSGTGPKEGAPGVGAGAGNAG 180
 QY 181 AAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAG 240
 DB 181 AAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAG 240
 QY 241 EVAFSHQKALPPDGHRRLDKI--EDERNLHED 272
 DB 241 EVAFSHQKALPPDGHRRLDKI--EDERNLHED 272
 QY 241 EVAFSHQKALPPDGHRRLDKI--EDERNLHED 272
 DB 241 EVAFSHQKALPPDGHRRLDKI--EDERNLHED 272
 RESULT 3
 TNFS_HUMAN STANDARD; PRT; 261 AA.
 ID TNFS_HUMAN
 AC P29965;

01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
CD40 LIGAND (CD40-L) (TNF-RELATED ACTIVATION PROTEIN) (TRAP) (T CELL
ANTIGEN GP39) (CD154 ANTIGEN).
TNFSF5 OR CD40LG OR CD40L OR TRAP.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
NCBI_Taxid=9606;
SEQUENCE FROM N.A.
MEDLINE-93076654; PubMed-1280226;
Graf D., Korthauer U., Mages H.W., Senger G., Kroczeck R.A.;
"Cloning of TRAP, a ligand for CD40 on human T cells.";
Eur. J. Immunol. 22:3191-3194(1992).
SEQUENCE FROM N.A.
MEDLINE-93049181; PubMed-1385114;
Hollenbaugh D., Grosmaire L.S., Kullas C.D., Chalupny J.N.,
Braesch-Andersen S., Noelle R.J., Stamenkovic I., Ledbetter J.A.,
Aruffo A.;
"The human T cell antigen gp39, a member of the TNF gene family, is a
ligand for the CD40 receptor: expression of a soluble form of gp39
with B cell co-stimulatory activity.";
EMBO J. 11:4313-4321(1992).
SEQUENCE FROM N.A. AND VARIANTS HIGM1 128-ARG-GLY-129 AND PRO-235.
MEDLINE-93145330; PubMed-7678782;
Aruffo A., Farrington M., Hollenbaugh D., Li X., Milatovich A.,
Nonoyama S., Bajorath J., Grosmaire L.S., Stenamp R., Neubauer M.,
Roberts R.L., Noelle R.J., Ledbetter J.A., Francke U., Ochs H.D.;
"The CD40 ligand, gp39, is defective in activated T cells from
patients with X-linked hyper-IgM syndrome.";
Cell 72:291-300(1993).
SEQUENCE FROM N.A.
MEDLINE-93094757; PubMed-1281209;
Spriggs M.K., Armitage R.J., Strockbine L., Clifford K.N.,
Macculi B.M., Sato T.A., Maliszewski C.R., Fanslow W.C.;
"Recombinant human CD40 ligand stimulates B cell proliferation and
immunoglobulin E secretion.";
J. Exp. Med. 176:1543-1550(1992).
SEQUENCE FROM N.A.
MEDLINE-93138085; PubMed-7678552;
Gauchat J.F.M., Aubry J., Mazzei G.J., Life P., Jomotte T., Elson G.,
Bonney J.Y.;
"Human CD40-ligand: molecular cloning, cellular distribution and
regulation of expression by factors controlling IgE production.";
FEBS Lett. 315:259-266(1993).
SEQUENCE FROM N.A.
Shimada M., Terasaki H., Ninomiya R., Shimizu S., Nunoi H.,
Matsuda I.;
Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 116-261.
MEDLINE-96131874; PubMed-8589998;
Karpusas M., Hsu Y.-M., Wang J.-H., Thompson J., Lederman S.,
Chen L., Thomas D.;
"2-A crystal structure of an extracellular fragment of human CD40
ligand.";
Structure 3:1031-1039(1995).
3D-STRUCTURE MODELING OF COMPLEX WITH CD40.
MEDLINE-9826353; PubMed-9605317;
Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M.,
Zheng Z., Naimith J.H., Thomas D.;
"The role of polar interactions in the molecular recognition of CD40L
with its receptor CD40.";
Protein Sci. 7:1124-1135(1998).
[9]

VARIANTS HIGM1 ARG-36 AND GLY-140.
MEDLINE-93156839; PubMed-7679206;
Korthauer U., Graf D., Mages H.W., Briere F., Padayachee M.,
Malcolm S., Ugaz A.G., Notarangelo L.D., Levinsky R.J.,
Kroczeck R.A.;
"Defective expression of T-cell CD40 ligand causes X-linked
immunodeficiency with hyper-IgM.";
Nature 361:539-541(1993).
VARIANT HIGM1 GLU-123.
MEDLINE-93156840; PubMed-8094231;
Disanto J.P., Bonney J.Y., Gauchat J.F.M., Fischer A.,
de Saint Basile G.;
"CD40 ligand mutations in X-linked immunodeficiency with hyper-IgM.";
Nature 361:541-543(1993).
VARIANTS HIGM1 PRO-155, ASP-211 AND VAL-227.
MEDLINE-93174270; PubMed-7679801;
Allen R.C., Armitage R.J., Conley M.E., Rosenblatt H., Jenkins N.A.,
Copeland N.G., Bedell M.A., Edelhoff S., Distcheck C.M.,
Simoneaux D.K., Fanslow W.C., Belmont J.W., Spriggs M.K.;
"CD40 ligand gene defects responsible for X-linked hyper-IgM
syndrome.";
Science 259:990-993(1993).
VARIANTS HIGM1 ALA-126; ARG-140 AND GLU-144.
MEDLINE-95233438; PubMed-7717401;
Macchi P., Villa A., Strina D., Sacco M.G., Morali F., Brugnani D.,
Gillani S., Mantuano E., Fasth A., Andersson B., Zegers B.J.M.,
Cavagni G., Reznik I., Levy J., Zan-Bar I., Porat Y., Alto P.,
Pleban G.A., Vezoni P., Notarangelo L.D.;
"Characterization of nine novel mutations in the CD40 ligand gene in
patients with X-linked hyper IgM syndrome of various ancestry.";
Am. J. Hum. Genet. 56:898-906(1995).
VARIANTS HIGM1 PRO-155 AND VAL-227, AND VARIANT ARG-219.
MEDLINE-96133533; PubMed-8550833;
Lin O., Rohrer J., Allen R.C., Larche M., Greene J.M., Shigeoka A.O.,
Gatti R.A., Derauf D.C., Belmont J.W., Conley M.E.;
"A single strand conformation polymorphism study of CD40 ligand.
Efficient mutation analysis and carrier detection for X-linked hyper
IgM syndrome.";
J. Clin. Invest. 97:196-201(1996).
VARIANTS HIGM1 ARG-36; CYS-140; SER-231; MET-254 AND GLY-227 DEL.
MEDLINE-97295077; PubMed-9150729;
Nonoyama S., Shimada M., Toru H., Seyama K., Nunoi H., Neubauer M.,
Yata J.-I., Ochi H.D.;
"Mutations of the CD40 ligand gene in 13 Japanese patients with
X-linked hyper-IgM syndrome.";
Hum. Genet. 99:624-627(1997).
FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-
STIMULUS AS WELL AS IGE PRODUCTION IN THE PRESENCE OF IL-4.
INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING.
SUBUNIT: HOMOTRIMER.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
EXTRACELLULAR SOLUBLE FORM.
TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED ON ACTIVATED CD4+
T-LYMPHOCYTES.
DISEASE: DEFECTS IN CD40LG ARE THE CAUSE OF AN X-LINKED
IMMUNODEFICIENCY WITH HYPER-IGM (HIGM1). AN IMMUNOGLOBULIN ISOTYPE
SWITCH DEFECT CHARACTERIZED BY ELEVATED CONCENTRATIONS OF SERUM
IGM AND DECREASED AMOUNTS OF ALL OTHER ISOTYPES. AFFECTED MALES
PRESENT AT AN EARLY AGE (USUALLY WITHIN THE FIRST YEAR OF LIFE)
RECURRENT BACTERIAL AND OPPORTUNISTIC INFECTIONS, INCLUDING
PNEUMOCYSTIS CARINII PNEUMONIA AND INTRACTABLE DIARRHEA DUE TO
CRYPTOSPORIDIM INFECTION. DESPITE SUBSTITUTION TREATMENT WITH
INTRAVENOUS IMMUNOGLOBULIN, THE OVERALL PROGNOSIS IS RATHER POOR,
WITH A DEATH RATE OF ABOUT 10% BEFORE ADOLESCENCE.
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
-1- DATABASE: NAME-CD40LBASE;
NOTE-EUROPEAN CD40L defect database (mutation db);
WWW="http://www.expasy.ch/cd40lbase/";
CC

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CC CC FTP:"ftp://ftp.expasy.ch/databases/cdd01base".
CC CC -I DATABASE: NAME=PROV; NOTE=CD guide CD154 entry;
CC CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd154.htm".
CC CC -----
CC CC This SWISS-Prot entry is copyright. It is produced through a collaboration
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CC CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC CC or send an email to licensel@sb.slb.ch).
-----
DR DR EMBL: X68590; CAA48554.1; -
DR DR EMBL: Z15017; CAA78737.1; -
DR DR EMBL: X67878; CAA48077.1; -
DR DR EMBL: L07444; AAA35662.1; -
DR DR EMBL: D31797; BAA06599.1; -
DR DR EMBL: D31793; BAA06599.1; JOINED.
DR DR EMBL: D31795; BAA06599.1; JOINED.
DR DR EMBL: D31796; BAA06599.1; JOINED.
DR DR PIR: S25684; S25684.
DR DR PIR: S26694; S26694.
DR DR PIR: S28017; S28017.
DR DR PIR: S28852; S28852.
DR DR PIR: JH0793; JH0793.
DR DR PDB: 1ALY; 17-SEP-97.
DR DR MIM: 308230; -.
DR DR InterPro: IPR000478; -.
DR DR Pfam: PF00228; TNE_1.
DR DR PROSITE: PS00251; TNE_1; 1.
DR DR PROSITE: PS50049; TNE_2; 1.
KW KW Cytochrome; Transmembrane; Glycoprotein; Signal-anchor; 3D-structure;
KM Disease mutation; polymorphism.
FT FT DOMAIN 1 22
FT FT TRANSMEM 23 46
FT FT CYTOPLASMIC (POTENTIAL).
FT FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT FT (POTENTIAL).
FT FT EXTRACELLULAR (POTENTIAL).
FT FT POTENTIAL.
FT FT N-LINKED (GLCNAC... ) (POTENTIAL).
FT FT M->R (IN HIGM1).
FT FT /FTID-VAR.007513.
FT FT A->E (IN HIGM1).
FT FT /FTID-VAR.007514.
FT FT V->A (IN HIGM1).
FT FT /FTID-VAR.007515.
FT FT SE->RG (IN HIGM1).
FT FT /FTID-VAR.007516.
FT FT W->C (IN HIGM1).
FT FT /FTID-VAR.007517.
FT FT W->G (IN HIGM1).
FT FT /FTID-VAR.007518.
FT FT VARIANT 140 140
Query Match 44.6%; Score 1110; DB 1; Length 261;
Best Local Similarity 100.0%; Pred.No.3..3e-55;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db Db 47 HRRLDKIDERNLHDEVFEMKTIQRCNTGRSLILNLCCEIKSPFEGGVKDIMLNKEETK 316
|||
Db Db 107 KENSFEOMKGQONPOIAAHAVISEASSKTSVLQMAEKGYTMSNNLYTLLENGKULTVARQ 166
|||
Db Db 377 GLYYIVAQWTFCSNRREASSOAPFIASICKLSGREGRRILLRAANTSSARPFGOSITHLG 436
|||
Db Db 167 GLYYIVAQWTFCSNRREASSOAPFIASICKLSGREGRRILLRAANTSSARPFGOSITHLG 436
|||
Db Db 437 GVVELDGASVFNVTDPDSQVSHGTSGFLKL 471
|||
Db Db 227 GVVELDGASVFNVTDPDSQVSHGTSGFLKL 261
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RESULT 4
PSPD_HUMAN
ID PSPD_HUMAN STANDARD; PRT: 375 AA.
AC P35247;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PULMONARY SURFACTANT-ASSOCIATED PROTEIN D (SP-D) (PSP-D)
GN SFTPD OR SFTPA OR PSPD.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=91315122; PubMed=8428971;
RA Crouch E., Rust K., Velle R., Denis-Keller H., Grosso L.;
RT "Genomic organization of human surfactant protein D (SP-D). SP-D is
RT encoded on chromosome 10q22.2-23.1.";
RL J. Biol. Chem. 268:2976-2983(1993).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 214-243.
RC TISSUE=Lung, and Amniotic fluid;
RX MEDLINE=92322003; PubMed=1339264;
RA Lu J., Willis A.C., Reid K.B.M.;
RT "Purification, characterization and cDNA cloning of human lung
RT surfactant protein D.";
RL Biochem. J. 284:795-802(1992).
RN [3]
RP SEQUENCE OF 60-375 FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=91378578; PubMed=1898081;
RA Rust K., Grosso L., Zhang V., Chang D., Persson A., Longmore W.,
RA Cai G.-Z., Crouch E.;
RT "Human surfactant protein D: SP-D contains a C-type lectin
RT carbohydrate recognition domain.";
RL Arch. Biochem. Biophys. 290:116-126(1991).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=99197291; PubMed=10368295;
RA Hakansson K., Lim N.K., Hoppe H.-J., Reid K.B.M.;
RT "Crystal structure of the trimeric alpha-helical coiled-coil and the
RT three lectin domains of human lung surfactant protein D.";
RL Structure 7:255-264(1999).
RN -1-
RP FUNCTION: CONTRIBUTES TO THE LUNG'S DEFENSE AGAINST INHALED
RP MICROORGANISMS. BINDS STRONGLY MALTOSE RESIDUES AND TO A LESSER
RP EXTENT OTHER ALPHA-GLUCOSYL MOTETIES. IT COULD PARTICIPATE IN THE
RP EXTRACELLULAR REORGANIZATION OR TURNOVER OF PULMONARY SURFACTANT.
RN -1-
RP SUBCELLULAR LOCATION: EXTRACELLULAR.
RN -1-
RP MISCELLANEOUS: PULMONARY SURFACTANT CONSISTS OF 90% LIPID AND 10%
RP CARBOHYDRATE-BINDING GLYCOPROTEINS (SP-A AND SP-D) AND 2 SMALL
RP HYDROPHOBIC PROTEINS (SP-B AND SP-C).
RN -1-
RP SIMILARITY: CONTAINS A COLLAGENOUS DOMAIN.
RN -1-
RP SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
RN -1-
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RP or send an email to license@sib-sib.ch).
RN -1-
RP EMBL: L05485; AAB59450.1;
RN -1-
RP EMBL: L05483; AAB59450.1; JOINED.
RN -1-
RP EMBL: L05484; AAB59450.1; JOINED.
RN -1-
RP EMBL: X65018; CAA6152.1;
RN -1-
RP PIR: A45225; A45225.
RN -1-
RP PIR: S18382; S18382.

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PDB: 1B08; 29-NOV-99.
 DR MIM; 178635; -.
 DR InterPro: IPR000087; -.
 DR InterPro: IPR001304; -.
 DR Pfam: PF01391; Collagen; 3.
 DR Pfam: PF00059; lectin; 1.
 DR PROSITE: PS00615; C-TYPE LECTIN-2; 1.
 DR PROSITE: PS50041; C-TYPE LECTIN-2; 1.
 DR Glycoprotein; Calcium; Surface film; Gaseous exchange; Hydroxylation;
 KW Signal; Lectin; Collagen; Repeat; Coiled coil; 3D-structure.
 FT SIGNAL 1 20
 FT CHAIN 21 375
 FT DOMAIN 46 222
 FT DOMAIN 223 252
 FT DOMAIN 279 375
 FT DISULFID 281 373
 FT DISULFID 351 365
 FT MOD_RES 721 721
 FT CARBOHYD 90 90
 FT MOD_RES 78 78
 FT MOD_RES 87 87
 FT MOD_RES 96 96
 FT MOD_RES 99 99
 FT MOD_RES 171 171
 FT MOD_RES 177 177
 FT CONFLICT 31 31
 FT CONFLICT 59 59
 FT CONFLICT 122 122
 FT CONFLICT 180 180
 FT CONFLICT 206 206
 FT CONFLICT 374 374
 FT SEQUENCE 375 AA: 37702 MW: 2986B26599FC01A6A CMC64;
 Query Match 42.3%; Score 1053; DB 1; Length 375;
 Best Local Similarity 72.6%; Pred. No. 6,7e-52;
 Matches 191; Conservative 28; Mismatches 44; Indels 0; Gaps 0;
 QY 1 MLPLSLMLVLLVOPICNLGAEMKSLSORSVPTCTLVCSPTENGLPGRDGRGREGPRG 60
 DB 2 LFLSLAVLLTOPICLGLAEKMTYSHRTMPACTLVCSVESGLPGRDGRGREGPRG 61
 QY 61 EKGDCGLPROMLSLGLQPTGPGPKGNSAGSRGPKGREGSLSPRLPGTPAGAKG 120
 DB 62 EKGDCGLPFAAGQAGPAGGAPVPGKDNQSVGPRGDPGPPGPGVAGAGRG 121
 QY 121 PSKGNIGIPQKPKGKGEVAPGMOGSGTGAKSGTGPKGERGAPVQAGPAGNAG 180
 DB 122 ALGKGNIGIPQKPKGKGEVAPGMOGSGTGAKSGTGPKGERGAPVQAGPAGNAG 181
 QY 181 AAGPAGPAGPQAGPAGSRGPGGLGKDRGVPDGRGIGKSGSLPDSALROOMALKGLQL 240
 DB 182 AAGSAGAGPQSGPAGRGPGGLGKDKGIPGDKAKGSGGLDVASLRQVEALQGVQVHL 241
 QY 241 EVAFSHYKALFPGDGHRLDKI 263
 DB 242 QAAFSQYKVELFPNGQSVGEKI 264
 RESULT 5
 TNF5_BOVIN STANDARD; PRT; 261 AA.
 ID TNF5_BOVIN
 AC P51749;
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE 30-MAY-2000 (Rel. 39, Last annotation update)
 DE CD40 LIGAND (TNF-RELATED ACTIVATION PROTEIN) (TRAP) (T CELL ANTIGEN GP39).
 GN TNF5 OR CD40LG OR CD40L.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.
 OK NCBI_TaxID=9913;
 RN 11
 RP SEQUENCE FROM N.A.
 RC TISSUE-Blood;
 RX MEDLINE=96006582; PubMed=7590981;
 RA Mertens B.E.L.C., Murtuki M., Gaidulis L.;
 RT "Cloning of two members of the TNF-superfamily in cattle: CD40 ligand
 and tumor necrosis factor alpha.";
 RL Immunogenetics 42:430-431(1995).
 CC -1- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-
 STIMULUS AS WELL AS IGE PRODUCTION IN THE PRESENCE OF IL-4.
 CC INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING (BY SIMILARITY).
 CC -1- SUBUNIT: HOMOTRIMER.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; Z48469; CAN8363.1; -.
 DR HSSP; P29965; IALT.
 DR InterPro: IPR00478; -.
 DR Pfam: PF00229; TNF; 1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS50049; TNF_2; 1.
 KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
 FT DOMAIN 1 22
 FT TRANSMEM 23 46
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT POTENTIAL.
 FT DOMAIN 47 261
 FT DISULFID 178 218
 FT CARBOHYD 240 240
 FT SEQUENCE 261 AA: 29242 MW: 8491FEF30A787ED CMC64;
 Query Match 39.2%; Score 974; DB 1; Length 261;
 Best Local Similarity 88.4%; Pred. No. 1.1e-47;
 Matches 190; Conservative 5; Mismatches 20; Indels 0; Gaps 0;
 QY 257 HRLDKIEDERNLHEDFVFPAKTIORCNTGERSLSLNCSEIKSOEGEVKIDMLNKEETK 316
 DB 47 HRLDKIEDERNLHEDFVFPAKTIORCNKKGESLSLNCSEIKSREDELYKIDMLNKEEVK 106
 QY 317 KENFEMKGDONPOIAAHVISEASSKTSYVLQNAEKGYTMSNNLVTLNCKQLTVKRO 376
 DB 107 KENFEMKGDONPOIAAHVISEASSKTSYVLQNAEKGYTMSNNLVTLNCKQLTVKRO 166
 QY 377 GLYTIYAQVTFCSNRAASSAPRTIASCLKSPGRPERILMAANTHSSAKPGQGSIHG 436
 DB 167 GFYIYITQVTFCSNRETLSQAPRTIASCLKSPSSSERILMAANTHSSAKPGQGSIHG 226
 QY 437 GVFELOPGASVFVNTDPSOVSHGTGFTSGLKL 471
 DB 227 GVFELOPGASVFVNTDPSOVSHGTGFTSGLKL 261
 RESULT 6
 PSPD_BOVIN STANDARD; PRT; 369 AA.
 ID PSPD_BOVIN
 AC P35246;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DE 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PULMONARY SURFACTANT-ASSOCIATED PROTEIN D PRECURSOR (SP-D) (PSP-D).
 GN SFTPD OR SFTP4.
 OS Bos taurus (Bovine).

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EMBL: X75911; CAA53510.1; -
PIR: S33603; S33603.
PSSD: n1000;

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interf; P19999; IMSB.
interPro; IPR0000087; -
interPro; IPR001304; -

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pfam: PF01391; Collagen; 3.
pfam: PF00059; Ictin_C/1.
PROSITE: PS00615; C type lectin; 1.

[illegible]

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SIGNAL	COLLAGEN; Repeat; Colled coll.	BY SIMILARITY.	exchange, hydroxylation;
SIGNAL			
CHAIN			

COLLAGEN-LIKE.	216	DOMAIN	46
CONTRACTANT-ASSOCIATED PROTEIN	248	DOMAIN	217
D.			

COMAIN	273
ISULEFD	369
ISULEFD	369
ISULEFD	367
ISULEFD	345
ISULEFD	350
BY SIMILARITY.	

	BY SIMILARITY.
90	N-LINKED (GLCNAC. . .) (POTENTIAL).
90	HYDROXYLATION (BY STRUTTER)
78	
78	
68	

Code	Description
87	HYDROXYLATION (BY SIMILARITY).
8/	HYDROXYLATION (BY SIMILARITY).
96	HYDROXYLATION (BY SIMILARITY).
99	HYDROXYLATION (BY SIMILARITY).
99	HYDROXYLATION (BY SIMILARITY).

COUENCH:		
DDRES	165	(BY SIMILARITY).
DDRES	171	HYDROXYLATION (BY SIMILARITY).
DDRES	171	HYDROXYLATION (BY SIMILARITY).
369 AA:	37361	MS. 07898222

Match 30 00 0/088824E0AEB2E3 CRC64;

Local Similarity	36.98;	Score 967.5;	DB 1;	Length 369;
es 193; Conservative	43;	Pred. No. 3.5e-47;	Mismatches 74.	Ratio 0.00

[illegible]

3 LIP-LSVLLLTQPMKSLGAEMKITYSQTKMANACTLVKCSPPEDGLPRDRGREGPRG 61
51 EKGDPLPGPMGI SGI OGPMCPMDRZKMA

[illegible]

Db	62	ENGDPGSPGPAGRAAMPGPAGPGLGKGDNGSAGEGPRGD---	7GPPGPPGMPGAPREG	118
OY	121	PSGKGNIGPGKGPSPKCEAGPKGIVGAPMGOSTAKSGTGPGERGAPGVOCAPNAG		160
Db	119	PSGKGNMGPGTTPROPKKDDTPKCGVAGAPGIQGS---	PGPAGLKGGERGAPGEFOAPBRAG	175
OY	181	AAGPAGPAGPQAGPQSGRCPGGLKGDRCVGPQIGKGGSSGPDENALROOMEALKGLQRL		240
Db	176	APGPAGLGPQGGSGANGPGLKGDRCPTPERKAKGSGSLAEVNALRORGLIGLQGLRL		235
OY	241	EVAFSHOKALFLPDGRRRDKTEDEENLHEDFVFKTTQRCNTG-----	EMS	288
Db	236	QNAFSQYTKKMLLPNGNSVGEK---FRYVQSEKTFQDQAQICQVAGOLPFRSGAENEA		293
OY	289	LSLLNCEIKSQEGEFKIDMLNKEEKKNSEEMQKQD	327	
Db	294	LTQLATAQNKAAL-----LSMSTTRPCCGMAK		

CONSIDERED IF IPICE 324

RESULT 7

TNF5_FELCA	STANDARD;	PRT;
ID		260 AA.
TNF5_FELCA		
AC		
097605.		

DT	01-OCT-2000 (Rel. 40, Created)
DT	01-OCT-2000 (Rel. 40, Last sequence undata)
DT	01-OCT-2000

CD40 LIGAND (CD154 ANTIGEN).
INFSF5 OR CD40LG OR CD40L.
CD40LG OR CD40L (Rel. 40, last annotation update)

Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Carnivora; Craniata; Vertebrata; Euteleostomi;

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99 NCBI_TaxID=9685;
100 NCBI_TaxID=9685;

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RC
Tissue=Thymus;
Hosie M.J., Willett B.J.;
RC

-I- FUNCTION: MEDISTES B-CELL PROLIFERATION

STIMULUS AS WELL AS IGE PRODUCTION IN THE ABSENCE OF CO-INVOLED IN IMMUNOGLOBULIN CLASS SWITCHING (BY SIMILARTY).

-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY)

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----- CREDIT TO licensee@sib.sib.ch).

EMBL: AF079105; AAD02954.1; -
HCCP: P0002E

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inter; P29965; ITALY.
InterPro; IPR000478; -
InterPro; IPR003263; -

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P1am: PF00229; TNF_1.
PROSITE: PS00251; TNF_1; 1.
PROSITE: PS50049; TNF_2; 1.

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TRANSMEM	DOMAIN	Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
1	22	CYTOPLASMIC (POTENTIAL)
2	2	

DOMAIN	23	46	47	260
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).				
EXTRACELLULAR (DOWNSTREAM)				

[illegible]

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      .          C99FA0391FB/B932 CRC64;
      .          37 00
Very Match

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est Local Similarity
57.8%; Score 939.5; DB 1; Length 260;
84.7%; Pred. No. 8.7e-46;

RA MEDLINE-87184551; PubMed-3566740.
 RT Young N.M., Leon M.A.:
 "The carbohydrate specificity of conglutinin and its homology to
 proteins in the hepatic lectin family";
 RL Biochem Biophys. Res. Commun. 143:645-651(1987).
 CC -1- FUNCTION: CALCIUM-DEPENDENT LECTIN-LIKE PROTEIN WHICH BINDS TO A
 CC COMPONENT (C3BI). IT IS CAPABLE OF BINDING NONREDUCING TERMINAL
 CC N-ACETYLGLUCOSAMINE, MANNOSE, AND FUCOSE RESIDUES.
 CC -1- SIMILARITY: CONTAINS A COLLAGENOUS DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: D14085; BAA03170.1; -
 DR EMBL: X11774; CA50665.1; -
 DR EMBL: L18871; AAA20126.1; -
 DR EMBL: U06860; AAB60624.1; -
 DR EMBL: U06854; AAB60624.1; -
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 DR EMBL: U06856; AAB60624.1; JOINED.
 DR EMBL: U06857; AAB60624.1; JOINED.
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 DR PIR: A29416; A29416.
 DR PIR: A23740; A23740.
 DR PIR: JN0450; JN0450.
 DR HSSP: P08651; JRM.
 DR InterPro: IPR000087; -
 DR InterPro: IPR001304; -
 DR Pfam: PF01391; Collagen; 3.
 DR Pfam: PF00059; Lectin; 1.
 DR PROSITE: PS00615; C-TYPE LECTIN_1; 1.
 DR PROSITE: PS50041; C-TYPE LECTIN_2; 1.
 KW Lectin; Hydroxylation; Glycoprotein; Mannose-binding; Membrane;
 KW Collagen; Repeat; Calcium; Signal.
 FT SIGNAL 1 20
 FT CHAIN 1 371
 FT DOMAIN 21 371 CONGLUTININ.
 FT MOD_RES 216 216 COLLAGEN-LIKE.
 FT MOD_RES 273 371 C-TYPE LECTIN (SHORT FORM).
 FT MOD_RES 63 63 HYDROXYLATION.
 FT MOD_RES 87 87 HYDROXYLATION.
 FT MOD_RES 99 99 HYDROXYLATION.
 FT MOD_RES 135 135 HYDROXYLATION.
 FT MOD_RES 141 141 HYDROXYLATION.
 FT MOD_RES 159 159 HYDROXYLATION.
 FT MOD_RES 162 162 HYDROXYLATION.
 FT MOD_RES 198 198 HYDROXYLATION.
 FT MOD_RES 203 203 HYDROXYLATION.
 FT SITE 201 203 CELL ATTACHMENT SITE (POTENTIAL).
 FT DISULFID 275 369 BY SIMILARITY.
 FT CARBOHYD 347 361 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 173 337 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 210 210 R -> H (IN REF. 2 AND 3).
 FT CONFLICT 218 218 V -> S (IN REF. 5).
 FT CONFLICT 272 272 E -> V (IN REF. 2).
 SO SEQUENCE 371 AA; 37994 MW; 867B4199254BIF CRC64;

Query Match 35.3%; Score 878; DB 1; Length 371;
 Best Local Similarity 49.5%; Pred. No. 3; le-42;
 Matches 180; Conservative 44; Mismatches 88; Indels 52; Gaps 6;

1 MLEPISMLVLYVLPGLNLAEMKSLQSRVPTCTLVMSPTENGIPGRGRGRGREGPG 60
 3 LIP-LSVILLLPWRSLQAEKMTTFSOKTIANACTLVMSPLSGLRGHGDGGRGRCPRG 61

QY 61 EKDGPGLPGMGLSLGTPGPGVPGKEGNSAGEPGRGERGLSGPPLPGIPACKREG 120
 DB 62 EKDPGSPGPRAGRGRGWRGPIGPKDNGFVGEPGKGD---TGPRGPRMGPRGREG 118
 QY 121 PSKRGQINGQGRGPRGGEAGPGEVGAAPMGOSTGAKGTGRGERGAPGVGAPGNAG 180
 DB 119 PSKQSGSMGPGTPGPGKGETGPGKGVGAPGQIO---GPPGSGLKGEGAPGAPGAPG 175
 QY 181 AAGPAPAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPG 240
 DB 176 VYGPSCALICPGPSPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPG 235
 QY 241 EVAFSHYGAALPPGGRHRLDKIEDERNLHEDFVFKTIORCNTGERSLNLNCEIRKQ 300
 DB 236 QNAFSQYKKAIVLPDQAVGEXI-----FKTAGAKSYSDAEOL-----CREAG- 280
 QY 301 FEGFVKDMLNKEETKENSPEMKGQDNPQIAHVISEASKTSVLOMEKGYTMSN 360
 DB 281 -----OLASPRSSAENEAIVQWVRAQEKNAVLSMN 310
 QY 361 NLVT 364
 DB 311 DIST 314
 RESULT 10
 ID TNFS_MOUSE STANDARD; PRT; 260 AA.
 AC P27548;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE CD40 LIGAND (TNF-RELATED ACTIVATION PROTEIN) (TRAP) (T CELL ANTIGEN GP39).
 GN TNFS5 OR CD40LG OR CD40L.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI-TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-9224364; PubMed-1374165;
 RA Armitage R., Fanslow W., Sato T.A., Clifford K.N., Strockbine L.,
 RA Macduff B.M., Anderson D.M., Gimpel S.D., Davis-Smith T.,
 RA Maliszewski C.R., Clark E.A., Smith C.A., Grabstein K.H., Cosman D.,
 RA Spriggs M.K.:
 RT "Molecular and biological characterization of a murine ligand for
 RT CD40.";
 RL Nature 357:80-82(1992).
 RN [2]
 RP SIMILARITY TO THE TNF FAMILY.
 RX MEDLINE-92310561; PubMed-1377364;
 RA Farrah T., Smith C.A.:
 RT "Emerging cytokine family.";
 RL Nature 358:26-26(1992).
 RN [3]
 RP 3D-STRUCTURE MODELING OF 115-260.
 RX MEDLINE-93200072; PubMed-8095800;
 RA Peltich M.C., Jongeneel C.V.:
 RA "A 3-D model for the CD40 ligand predicts that it is a compact trimer
 RT similar to the tumor necrosis factors.";
 RL J. Immunol. 152:233-238(1993).
 CC -1- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-
 CC STIMULUS AS WELL AS IGE PRODUCTION IN THE PRESENCE OF IL-4.
 CC INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING.
 CC -1- SUBUNIT: HOMOTRIMER.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
 CC EXTRACELLULAR SOLUBLE FORM.
 CC -1- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED ON ACTIVATED CD4+
 CC T-LIMPHOCYTES.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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 CC or send an email to license@sdb-sdb.ch).

DR EMBL: X65453; CAA46448.1; -
 DR PIR: S21738; S21738.
 DR PDB: 1CDA; 31-OCT-93.
 DR MGD: MGI:88337; Tnf8f5.
 DR InterPro: IPR000478; -
 DR Pfam: PF00229; Tnf; 1.
 DR PROSITE: PS00251; Tnf_1; 1.
 DR PROSITE: PS50049; Tnf_2; 1.
 DR Cytokine; Transmembrane; Glycoprotein; Signal anchor; 3D-structure.
 KW DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 23 46 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT DOMAIN 47 260 EXTRACELLULAR (POTENTIAL).
 FT DISULFID 177 217 (POTENTIAL).
 FT CARBOHYD 239 239 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 260 AA; 29396 MW; 7E0F34F7473668B7 CRC64;

Query Match 33.3%; Score 827; DB 1; Length 260;
 Best Local Similarity 64.8%; Pred. No. 1,4e-39;
 Matches 171; Conservative 29; Mismatches 52; Indels 12; Gaps 4;

QY 209 PGDRGKIGSGLPDSALRQOMELKGLKRL-EVAFSHYOKAALFPDGHRLKIEDER 267
 DB 8 PEPASV-ATGLPASKKIFMYLLVFLITQMGISLVFAVYL-----HRRDKVEEV 57
 QY 268 NIHEDFVFKTIQRCNTGERSLSLNCSEIKSQEGFYKIMLNKEFKKNSFEMOKGD 327
 DB 58 NIHEDFVFKTIQRCNTGERSLSLNCSEIKSQEGFYKIMLNKEFKKNSFEMOKGD 327
 QY 328 ONPQIAAHYISEASKTSTYLQNAEKGYTNSNLYLTENKQLTVKRGGLYYIAQVTF 387
 DB 117 EBPQIAAHYISEASKTSTYLQNAEKGYTNSNLYLTENKQLTVKRGGLYYIAQVTF 387
 QY 388 GSNREASSQAPFIASLCLKSPGRPERILLRANTHSSAKPGQOSILHGGVELOGASV 447
 DB 177 GSNREASSQAPFIASLCLKSPGRPERILLRANTHSSAKPGQOSILHGGVELOGASV 447
 QY 448 FVNTDPSQVSHGCTFTSFCGLKL 471
 DB 237 FVNTDPSQVSHGCTFTSFCGLKL 260

RESULT 11
 CL43_BOVIN STANDARD; PRT; 301 AA.
 AC P42916;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE COLLECTIN-43 (CL-43).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 JOX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=94216283; Pubmed=8163480;
 RA Lim B.-L., Willis A.C., Reid K.B.M., Lu J., Laursen S.B.,
 RA Jensenius J.C., Holmskov U.;
 RA *Primary structure of bovine collectin-43 (CL-43). Comparison with
 RA conglutinin and lung surfactant protein-D.*;
 RT J. Biol. Chem. 269:11820-11824(1994).

CC -1- FUNCTION: LECTIN THAT BINDS TO VARIOUS SUGARS. MANNOSIDE - MANNAC >
 CC FUCOSE > GLCNAC > GLUCOSE - MALTOSE > GALACTOSE > LACTOSE >
 CC GALNAC. COULD PLAY A ROLE IN IMMUNE DEFENSE.
 CC -1- SUBUNIT: OLIGOMERIC COMPLEX OF 4 SET OF HOMOTRIMERS.
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- SIMILARITY: CONTAINS A COLLAGENOUS DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
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DR EMBL: X75912; CAA53511.1; ALT_SEO.
 DR HSSP: P19999; 1MSB.
 DR InterPro: IPR000087; -
 DR InterPro: IPR001304; -
 DR Pfam: PF01391; Collagen; 2.
 DR Pfam: PF00059; Lectin; 1.
 DR PROSITE: PS00615; C-TYPE_LECTIN_1; 1.
 DR PROSITE: PS50041; C-TYPE_LECTIN_2; 1.
 DR Lectin; Hydroxylation; Glycoprotein; Mannose-binding; Collagen;
 KW Repeat; Calcium.
 KW DOMAIN 29 142 COLLAGEN-LIKE
 FT DOMAIN 202 301 C-TYPE LECTIN (SHORT FORM).
 FT DISULFID 204 299 BY SIMILARITY.
 FT DISULFID 277 291 BY SIMILARITY.
 SQ SEQUENCE 301 AA; 31362 MW; 0385C10B8424CD76 CRC64;

Query Match 22.7%; Score 565.5; DB 1; Length 301;
 Best Local Similarity 35.8%; Pred. No. 4.8e-25;
 Matches 127; Conservative 42; Mismatches 81; Indels 105; Gaps 8;

QY 21 EMKSLQSRVNPNTCTLYMCSPTENGLPGRGDRGREGRGEGDGLPQPMGLSLGCGPT 80
 DB 2 EMDVYSEKTLTDCCTLVCAFPADSLRGHGRDKEGEGGEGDGP----- 46
 QY 81 GPVPGKMGNSAGPEPGKGRGLSGPGLPGIPGAPKRGSGKONIGPOGKPGKGEA 140
 DB 47 -----GPPGM-----PGPAGREGSGRSGSNKPGPTGPKGEP 79
 QY 141 GPKGEVAGAPMGOSTGKSGTGPKGERGAPGVOCAPGNAGAAGPAGPAGPAGSRGP 200
 DB 80 GPEGGVAGAPMGPS---GPGAAGLGERGAP-----GPGAAGPAGPAGSRGP 124
 QY 201 GLKDRGVDPDRGKIGSGSLPDSALRQOMELKGLKRLLEVAFSHYOKAALFPDGHRL 260
 DB 125 GLKDRGVDPDRGKIGSGSLPDSALRQOMELKGLKRLLEVAFSHYOKAALFPDGHRL 260
 QY 261 DKIEDERNLHEDFVFKTIQRCNTGERSLSLNCSEIKSQ-----EGF 304
 DB 185 EKI-----FKTAGVAKSYSDAEOL-----CREAKQLASPRSSAENAVTQLVRAK 230
 QY 305 VQDMLNKEETKKNSFEMOKG-----DONPOIAHVISAS 341
 DB 231 NKHAYLSMNDISKEGFTYPTGSLDYSNMAPGERGNRAKDEGPENCLEIYSDGN 285

RESULT 12
 CAL3_BOVIN STANDARD; PRT; 1049 AA.
 ID CAL3_BOVIN
 AC P04258;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 20-MAR-1987 (Rel. 04, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE COLLAGEN ALPHA 1(I111) CHAIN.
 GN COL3A1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 RX NCBI_TaxID=9913;
 RX [1]
 RX SEQUENCE OF 1-242.
 RX MEDLINE=80026026; PubMed=488906;
 RA Fietzek P.P., Allmann H., Rautenberg J., Henkel W., Wachter E.,
 RA Kuhn K.;
 RT "The covalent structure of calf skin type I collagen. I. The amino
 RT acid sequence of the amino terminal region of the alpha 1(I) chain
 RT (positions 1-222).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 360:809-820(1979).
 RN [2]
 RX SEQUENCE OF 243-422.
 RX MEDLINE=80026027; PubMed=488907;
 RA Dewes H., Fietzek P.P., Kuhn K.;
 RT "The covalent structure of calf skin type III collagen. II. The amino
 RT acid sequence of the cyanogen bromide peptide alpha 1(III)CBI,8,10,2
 RT (positions 223-402).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 360:833-840(1979).
 RN [3]
 RX SEQUENCE OF 423-571.
 RX MEDLINE=80026028; PubMed=488908;
 RA Bentz H., Fietzek P.P., Kuhn K.;
 RT "The covalent structure of calf skin type III collagen. III. The
 RT amino acid sequence of the cyanogen bromide peptide alpha 1(III)CB4
 RT (positions 403-551).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 360:851-860(1979).
 RN [4]
 RX SEQUENCE OF 572-808.
 RX MEDLINE=80026029; PubMed=488909;
 RA Lang H., Glanville R.W., Fietzek P.P., Kuhn K.;
 RT "The covalent structure of calf skin type III collagen. IV. The amino
 RT acid sequence of the cyanogen bromide peptide alpha 1(III)CB5
 RT (positions 552-788).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 360:841-850(1979).
 RN [5]
 RX SEQUENCE OF 809-947.
 RX MEDLINE=80026030; PubMed=488910;
 RA Dewes H., Fietzek P.P., Kuhn K.;
 RT "The covalent structure of calf skin type III collagen. V. The amino
 RT acid sequence of the cyanogen bromide peptide alpha 1(III)CB9A
 RT (positions 789-927).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 360:851-860(1979).
 RN [6]
 RX SEQUENCE OF 948-1049.
 RX MEDLINE=80026031; PubMed=488911;
 RA Allmann H., Fietzek P.P., Glanville R.W., Kuhn K.;
 RT "The covalent structure of calf skin type III collagen. VI. The amino
 RT acid sequence of the carboxyterminal cyanogen bromide peptide alpha
 RT 1(III)CB9B (positions 928-1028).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 360:861-868(1979).
 RN [7]
 RX FUNCTION: COLLAGEN TYPE III OCCURS IN MOST SOFT CONNECTIVE TISSUES
 RX ALONG WITH TYPE I COLLAGEN.
 RX -1- SUBUNIT: TRIMERS OF IDENTICAL ALPHA 1(III) CHAINS. THE CHAINS ARE
 RX LINKED TO EACH OTHER BY INTERCHAIN DISULFIDE BONDS. TRIMERS ARE
 RX ALSO CROSS-LINKED VIA HYDROXYLYSINES.
 RX -1- UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
 RX PIR: A02862; CG8075.
 DR InterPro: IPR001007;
 DR Pfam: PF01391; Collagen: 17.
 DR PROSITE: PS01208; VWF; PARTIAL.
 KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
 FT DOMAIN 1 14 NONHELICAL REGION (N-TERMINAL).
 FT DOMAIN 15 1040 TRIPLE-HELICAL REGION.
 FT MOD_RES 1041 1049 NONHELICAL REGION (C-TERMINAL).
 FT MOD_RES 95 95 HYDROXYLYATION.
 FT MOD_RES 107 107 HYDROXYLYATION.
 FT MOD_RES 119 119 HYDROXYLYATION.
 FT MOD_RES 938 938 HYDROXYLYATION.

Query Match 19.5%; Score 484.5; DB 1; Length 1049;
 Best Local Similarity 41.2%; Pred. No. 5.2e-20;
 Matches 113; Conservative 13; Mismatches 71; Indels 77; Gaps 9;
 FT MOD_RES 950 950 HYDROXYLYATION.
 FT CARBOHYD 107 107 CROSS-LINK SITE.
 FT CARBOHYD 950 950 CROSS-LINK SITE.
 FT DISULFID 1040 1040 INTERCHAIN.
 FT DISULFID 1041 1041 INTERCHAIN.
 SQ SEQUENCE 1049 AA; 93651 MW; 8EEC33D1C66EC9A3 CRC64;
 QY 14 PLGNIGAEKKSLSORVPTCTLMCSPTENGILGRGRGRF-----GPRKGDPL 67
 DB 427 PKGNDAPEKN-GERGPG-----GPGPGAGKNGETGPGPGPSDKDGTGP 478
 QY 68 PGPGLSGIQTGTPVGPENGSGASGEPGKRGEL-----SGPPLPGI 112
 DB 479 PGPGGLGLPGTS--GPPGKRGEPGPGKGAAPGIPGKCDSGAPGEPGPGAGP 535
 QY 113 PGPAGKSPSKGKGNIGPGKPGKEA-----GPGKGVAGPMGS 154
 DB 536 PGPAGAPPPGPGGKGAAPPGPSAGTPGLQGMPERGPGPGPGKGGEGSSGV 595
 QY 155 TGKSGTGP-----KGERGAPV-----QAPGNAGAAGPAPAP 190
 DB 596 DGAPKDGPRGPTGPICPPAPAGPGKSGAPGVPCIAPRGPGGPGGPGPAGP 655
 QY 191 QGAPGSRPGKDKDRVPPGDRGKSGGLPDSA 224
 DB 656 PGAPGONGEPGANGEPAGE--KGECPGPA 686
 RESULT 13
 ID CALL_CANFA STANDARD; PRT: 1460 AA.
 AC Q9XSJ7;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE COLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
 OS Canis familiaris (dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 RX NCBI_TaxID=9615;
 RX [1]
 RX SEQUENCE FROM N.A.
 RX TISSUE=Skin;
 RA Campbell B.G., Wootton J.A.M., McLeod J.N., Minor R.R.;
 RT "Sequence of normal canine COL1A1 cDNA.";
 RT Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: TYPE I COLLAGEN IS A MEMBER OF GROUP I COLLAGEN
 CC (FIBRILLAR FORMING COLLAGEN).
 CC -1- SUBUNIT: TRIMERS OF ONE ALPHA 2(I) AND TWO ALPHA 1(I) CHAINS.
 CC -1- UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
 CC -1- SIMILARITY: CONTAINS 1 VWF DOMAIN.
 CC -----
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 CC -----
 DR EMBL: AF153062; A034619.1;
 DR InterPro: IPR000885;
 DR InterPro: IPR001007;
 DR Pfam: PF01410; COLF1; 1.
 DR PROSITE: PS01208; VWF; 1.
 KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;

[13]
 RP REVIEW ON OI VARIANTS.
 RX MEDLINE-97169389; PubMed-9016532;
 RA Dalglish R.;
 RT "The human type I collagen mutation database.";
 RL Nucleic Acids Res. 25:181-187(1997).
 RN [14]
 RP VARIANT OI-II CYS-1166.
 RX MEDLINE-86287390; PubMed-3016737;
 RA Cohn D.H., Byers P.H., Steinmann B., Gellinas R.E.;
 RT "Lethal osteogenesis imperfecta resulting from a single nucleotide
 change in one human pro alpha 1(I) collagen allele.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:6045-6047(1986).
 RN [15]
 RP VARIANT OI-II ARG-569.
 RX MEDLINE-87222295; PubMed-3108247;
 RA Bateman J.F., Chan D., Walkers I.D., Rogers J.G., Cole W.G.;
 RT "Lethal perinatal osteogenesis imperfecta due to the substitution of
 arginine for glycine at residue 391 of the alpha 1(I) chain of type I
 collagen.";
 RL J. Biol. Chem. 262:7021-7027(1987).
 RN [16]
 RP VARIANT OI-II CYS-926.
 RX MEDLINE-88033031; PubMed-3667599;
 RA Vogel B.E., Minor R.R., Freund M., Prockop D.J.;
 RT "A point mutation in a type I procollagen gene converts glycine 748
 of the alpha 1 chain to cysteine and destabilizes the triple helix in
 a lethal variant of osteogenesis imperfecta.";
 RL J. Biol. Chem. 262:14737-14744(1987).
 RN [17]
 RP VARIANT OI-II ARG-842.
 RX MEDLINE-88298828; PubMed-3403550;
 RA Bateman J.F., Lamande S.R., Dahl H.H., Chan D., Cole W.G.;
 RT "Substitution of arginine for glycine 664 in the collagen alpha 1(I)
 chain in lethal perinatal osteogenesis imperfecta. Demonstration of
 the peptide defect by in vitro expression of the mutant cDNA.";
 RL J. Biol. Chem. 263:11627-11630(1988).
 RN [18]
 RP VARIANT OI CYS-1195.
 RX MEDLINE-89218628; PubMed-3244312;
 RA Labhard M.E., Wirtz M.K., Pope F.W., Nicholls A.C., Hollister D.W.;
 RT "A cysteine for glycine substitution at position 1017 in an alpha
 1(I) chain of type I collagen in a patient with mild dominantly
 inherited osteogenesis imperfecta.";
 RL Mol. Biol. Med. 5:197-207(1988).
 RN [19]
 RP VARIANT OI-II VAL-434.
 RX MEDLINE-8925493; PubMed-2470760;
 RA Patterson E., Smiley E., Bonadio J.;
 RT "RNA sequence analysis of a perinatal lethal osteogenesis imperfecta
 mutation.";
 RL J. Biol. Chem. 264:10083-10087(1989).
 RN [20]
 RP VARIANT OI-IV SER-1010.
 RX MEDLINE-89308591; PubMed-2745420;
 RA Marini J.C., Grange D.K., Gottesman G.S., Lewis M.B., Koepflin D.A.;
 RT "Osteogenesis imperfecta type IV. Detection of a point mutation in
 one alpha 1(I) collagen allele (COL1A1) by RNA/RNA hybrid analysis.";
 RL J. Biol. Chem. 264:11893-11900(1989).
 RN [21]
 RP VARIANTS OI-II ALA-1106; VAL-1151; ARG-1154 AND VAL-1184.
 RX MEDLINE-89380165; PubMed-2777764;
 RA Lamande S.R., Dahl H.H.M., Cole W.G., Bateman J.F.;
 RT "Characterization of point mutations in the collagen COL1A1 and
 COL2 genes causing lethal perinatal osteogenesis imperfecta.";
 RL J. Biol. Chem. 264:15809-15812(1989).
 RN [22]
 RP VARIANT OI SER-1022.
 RX MEDLINE-90062068; PubMed-2511192;
 RA Pack M., Constantinou C.D., Kalia K., Nielsen K.B., Prockop D.J.;
 RT "Substitution of serine for alpha 1(I)-glycine 844 in a severe
 variant of osteogenesis imperfecta minimally destabilizes the triple
 helix of type I procollagen. The effects of glycine substitutions on
 thermal stability are either position of amino acid specific.";
 RL J. Biol. Chem. 264:19694-19699(1989).
 RN [23]
 RP VARIANT OI-II CYS-1082.
 RX MEDLINE-89109573; PubMed-2913053;
 RA Constantinou C.D., Nielsen K.B., Prockop D.J.;
 RT "A lethal variant of osteogenesis imperfecta has a single base
 mutation that substitutes cysteine for glycine 904 of the alpha 1(I)
 chain of type I procollagen. The asymptomatic mother has an
 unidentified mutation producing an overmodified and unstable type I
 procollagen.";
 RL J. Clin. Invest. 83:574-584(1989).
 RN [24]
 RP VARIANT OI CYS-272; CYS-704 AND CYS-896.
 RX MEDLINE-90009313; PubMed-2794057;
 RA Staman B.J., Eyré D., Charbonneau H., Harrylock M., Wels M.A.,
 RT "Wels L., Graham J.M., Byers P.H.;
 RT "Osteogenesis imperfecta. The position of substitution for glycine by
 cysteine in the triple helical domain of the pro alpha 1(I) chains of
 type I collagen determines the clinical phenotype.";
 RL J. Clin. Invest. 84:1206-1214(1989).
 RN [25]
 RP VARIANT OI-II CYS-422.
 RP
 Query Match 19.4%; Score 481.5; DB 1; Length 1464;
 Best Local Similarity 41.6%; Pred. No. 1.1e-19;
 Matches 112; Conservative 9; Mismatches 77; Indels 71; Gaps 7;
 OY 14 PLGNLGAEMKSLRSRSPNTCTLYMCSPTEENGLPGRCRDREPRGKXGDPGLPGL 73
 DB 852 PIGNVGA PKAGKAGAGSG-----PPGATGFGAGAGRGVPPSPNAGPBPAGK 903
 OY 74 SGIGGPTGPGVPGKENGMSAGEPGP-----KGENGLSGPGLGPIGP----- 115
 DB 904 EGKGGRGEGTGPAGRGVEGPPPPGPKGSGPADGAPGAGTGPQGITAGRGVYGL 963
 OY 116 -----AGKGPSSGKGNITGPGRPGPGEAGPGE-----VGA 148
 DB 964 PQGRGRGPGPLGPGSEPGKOGPGSCASGSGRPPGPGPLAGPGESEGRGAPAEQS 1023
 OY 149 PQMGSTGAK---GSGTPKRGCAAPGVGAPGNAGA-----GPAAGPQGAPGS 196
 DB 1024 PQRDSPGAKGDPGRGEPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPG 1083
 OY 197 RGPPL-----KGRGVPGRGIRGIESG 219
 DB 1084 RGPAGPQGPGRDGRGEGDGRGIRGIRG 1112
 RESULT 15
 CAIL_CHICK STANDARD; PRT; 1453 AA.
 ID CAIL_CHICK
 AC P02457;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE COLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
 GN COL1A1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE OF 1-153 FROM N.A.
 RX MEDLINE-88056316; PubMed-3678834;
 RA Finer M.H., Boedtker H., Doty P.;
 RT "Construction and characterization of cDNA clones encoding the 5' end
 of the chicken pro alpha 1(I) collagen mRNA.";
 RL Gene 56:71-78(1987).
 RN [2]
 RP SEQUENCE OF 1-144 FROM N.A.
 RX MEDLINE-88007542; PubMed-2820966;

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GenCore version 4.5
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OM protein - protein search, using SW model

Run on: July 3, 2001, 16:14:38 ; Search time 25.5 seconds

(without alignments)
2443.752 Million cell updates/sec

Title: US-09-454-223-2
Perfect score: 2487
Sequence: 1 MPEFLSMVLVLOPLGNLGA.....TDPQVSHGTFGRFGLKL 471

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

SPTREMBL_16:*

- 1: SP-archaea:*
- 2: SP-bacteria:*
- 3: SP-fungi:*
- 4: SP-human:*
- 5: SP-invertebrate:*
- 6: SP-mammal:*
- 7: SP-mhc:*
- 8: SP-organelle:*
- 9: SP-phage:*
- 10: SP-plant:*
- 11: SP-rodent:*
- 12: SP-unclassified:*
- 13: SP-vertebrate:*
- 14: SP-virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1039.5	41.8	378	Q9N1X4	Q9N1X4 sus scrofa
2	836	33.6	260	Q922V2	Q922V2 rattus norv
3	827	33.3	260	Q9R254	Q9R254 rattus norv
4	697	28.0	335	Q97748	Q97748 bos taurus
5	499.5	20.1	890	Q77087	Q77087 alvinella p
6	488.5	19.6	888	Q90796	Q90796 gallus gall
7	488	19.6	1835	Q91A04	Q91A04 gallus gall
8	482.5	19.4	1445	Q93251	Q93251 rana catesb
9	481	19.3	1431	Q93JH4	Q93JH4 mesocricetu
10	480.5	19.3	1461	Q76045	Q76045 homo sapien
11	480.5	19.3	1838	Q88207	Q88207 mus musculu
12	480	19.3	1767	Q901T4	Q901T4 homo sapien
13	480	19.3	1806	Q901T5	Q901T5 homo sapien
14	479.5	19.3	1818	Q901T6	Q901T6 homo sapien
15	479.5	19.3	1838	Q15094	Q15094 homo sapien
16	479.5	19.3	1840	Q60467	Q60467 cricetus
17	479.5	19.3	1840	Q93103	Q93103 rattus norv
18	478.5	19.2	1453	Q63079	Q63079 rattus norv
19	478	19.2	1736	Q901P9	Q901P9 homo sapien

20	477.5	19.2	1450	13	Q911B4	Q911B4 cynops pyr
21	476	19.1	284	4	Q9UC14	Q9UC14 homo sapien
22	476	19.1	349	4	Q99018	Q99018 homo sapien
23	476	19.1	1497	4	Q9NCK9	Q9NCK9 homo sapien
24	476	19.1	1532	4	Q02802	Q02802 homo sapien
25	476	19.1	1739	11	Q9UL12	Q9UL12 mus musculu
26	475.5	19.1	1136	11	Q35053	Q35053 mus musculu
27	475.5	19.1	1418	13	Q9W7R9	Q9W7R9 cynops pyr
28	475	19.1	1160	4	Q14046	Q14046 homo sapien
29	475	19.1	1433	11	Q07563	Q07563 mus musculu
30	475	19.1	1497	4	Q9UMD9	Q9UMD9 homo sapien
31	473	19.0	1491	13	Q91718	Q91718 xenopus lae
32	472	19.0	1418	6	Q28396	Q28396 equus caball
33	472	19.0	1487	4	Q14047	Q14047 homo sapien
34	472	19.0	1487	6	Q77753	Q77753 canis famill
35	472	19.0	1737	11	Q93104	Q93104 rattus norv
36	471.5	19.0	1447	13	Q91B91	Q91B91 xenopus lae
37	471	18.9	1486	13	Q91717	Q91717 xenopus lae
38	470.5	18.9	473	11	Q70605	Q70605 rattus norv
39	470	18.9	918	13	Q90583	Q90583 gallus gall
40	469.5	18.9	1442	11	Q62031	Q62031 mus musculu
41	469.5	18.9	1442	11	Q62033	Q62033 mus musculu
42	469.5	18.9	1459	11	Q62032	Q62032 mus musculu
43	469	18.9	886	13	Q92029	Q92029 gallus gall
44	468.5	18.8	1745	4	Q9NZ06	Q9NZ06 homo sapien
45	467.5	18.8	1142	4	Q13676	Q13676 homo sapien

ALIGNMENTS

RESULT	ID	Q9N1X4	PRELIMINARY:	PRT:	378 AA.
AC	Q9N1X4				
DT	01-OCT-2000	(TRENBLREL, 15, Created)			
DT	01-OCT-2000	(TRENBLREL, 15, Last sequence update)			
DT	01-MAR-2001	(TRENBLREL, 16, Last annotation update)			
DE	LUNG SURFACTANT PROTEIN D PRECURSOR.				
GN	SFTPD.				
OS	Sus scrofa (Pig).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.				
OX	NCBI_TaxID=9823;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-20109098; PubMed-10640760;				
RA	van Eljk M., Haagsman H.P., Skinner T., Archibald A.L., Reid K.B.M.,				
RT	Lawson P.R.;				
RT	*Porcine Lung Surfactant Protein D (SP-D): cDNA cloning, chromosomal				
RL	localisation and tissue distribution.*;				
DR	J. Immunol. 164:1442-1450(2000).				
DR	EMBL: AF132496; AAF22145.2; .				
DR	InterPro: IPR000087; .				
DR	InterPro: IPR001304; .				
DR	Pfam: PF000059; Lectin_C; 1.				
DR	Pfam: PF01391; Collagen; 3.				
DR	PROSITE: PS00615; C-TYPE_LLECTIN_1; 1.				
DR	PROSITE: PS50041; C-TYPE_LLECTIN_2; 1.				
DR	SMART: SM00034; CLECT; 1.				
KW	Signal.				
FT	CHAIN	1	20	POTENTIAL.	
FT	CHAIN	21	378	LUNG SURFACTANT PROTEIN D.	
SO	SEQUENCE	378 AA;	37986 MW;	3504EBCE156C341D CAC64;	
QY	Query Match	41.8%;	Score 1039.5;	DB 6;	Length 378;
Db	Best Local Similarity	55.8%;	Pred. No. 3.5e-73;		
	Matches 218;	Conservative 38;	Mismatches 82;	Indels 53;	Gaps 8;
	1 MPEFLSMVLVLOPLGNLGAEMKSLRSRVNPTGLWCSPTENCLPGHDGDRGPRG 60				
	: : : : : : : : : :				
	3 LLP-LSVLLITROPSPSLGAEKMTYSQRAVANACALVWCSPMENCLPGRDGRGPRG 61				

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QY 61 EKDGPGLPGMGLSGLOCTGTPVGPKEGNGSGEPGPKGERLGGPPLGIPGPAGKEG 120
DB 62 EKGDPGLGAVGRAGMPLAGVPGGNGSGTEGEGAGDIDPCGPPGPPGIPGPAKKEG 121
QY 121 PSOGNGNIGPQGPQKPGKEGAVGKMGSGTGAGSGTQPKERKAPGVQAGPAGNAG 180
DB 122 PSOGNGNIGPQGPQKPGKEGAVGKMGSGTGAGSGTQPKERKAPGVQAGPAGNAG 181
QY 181 AAGPAGPAGPQGPQKPGKEGAVGKMGSGTGAGSGTQPKERKAPGVQAGPAGNAG 240
DB 182 AAGPAGPAGPQGPQKPGKEGAVGKMGSGTGAGSGTQPKERKAPGVQAGPAGNAG 241
QY 241 EVAPSHYQKALFPDGHRRDLKEDERLHEDFYPMKTIC-----RCNT 284
DB 242 OKAFSGYKKEVLPNGRGVEKI-----KFGGEFTQDAQOYCTQAGGQMASPSET 295
QY 285 3ERSLNLNCEIKSQPEGVKDIMLNKEETKENSEFEMOKGONPQIAHVISSASKT 344
DB 296 EMBALSLQVTAOKKAF-----LSMTDICTEGNTPYTG-PLVYAN----- 336
QY 345 TSVLQMA-----EKGYTWSNNLVTL-ENGK 369
DB 337 -----WADGEPNNNGSSGACENCVEIFPNK 362

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RESULT 2
Q922V2 PRELIMINARY; PRT: 260 AA.
AC Q922V2;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DE CD40 LIGAND. 16, last annotation update)
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-EPG: TISSUE-SPLEEN;
RA Daniel K.C., Foss Y., Mousavi A., Macary P., Kenney D.M.,
RA Faranah F., Gaken J.A.;
RT "Cloning and sequencing of rat CD40 ligand."
RT Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF013985; AAD09323.1;
DR HSSP; P27548; ICDA.
DR InterPro: IPR000478;
DR InterPro: IPR003263;
DR Pfam: PF00229; TNF_1;
DR ProDom: PD008600; TNF_1;
DR PROSITE; PS00251; TNF_1;
DR PROSITE; PS00499; TNF_2;
DR SMART; SM00207; TNF_1;
SQ SEQUENCE 260 AA; 29282 MW; 15D21F5200FDEBB CRC64;

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Query Match: 33.6%; Score 836; DB 11; Length 260;
Best Local Similarity 65.5%; Pred. No. 1.5e-57;
Matches 173; Conservative 27; Mismatches 52; Indels 12; Gaps 4;
QY 209 PGDRCIKESGLPDSALRQOMELKGLQRL-EVAFSHYQKALFPDGHRRDLKEDER 267
DB 8 PPSRSV--ATGLPASKMIFVLLTFLITOMIGSVLFAVYL-----HRLDVEEBA 57
QY 268 NLHEDFVEMKTIORCNGERSLNLNCEIKSQPEGVKDIMLNKEETKENSEFEMOKG 327
DB 58 SLHEDFVFKKLRCKNGEGSLNLNCEIKSQPEGVKDIMLNKEETKENSEFEMOKG 116
QY 328 QNPQIAHVISSASKTTSVLOAENGKYTWSNNLVTLNKGKQLTVRKGLIYIYAQVF 387
DB 117 EDPQIAHVISSASKTTSVLOAENGKYTWSNNLVTLNKGKQLTVRKGLIYIYAQVF 176

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QY 388 CSNREASSOAPFLASLCLKSPGRRERILLRANTHSSAKPCGQOSIHGVEFLQPCASV 447
DB 177 CSNREPLSORPFLVSLMLKSSGSEERILLRANTHSSSKLCEQOSIHGVEFLQPCASV 236
QY 448 FNVVTDPSOVSHGTGFTSFGLTKL 471
DB 237 FNVVTEASQVHIGIGFSISGLTKL 260

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RESULT 3
Q9R254 PRELIMINARY; PRT: 260 AA.
AC Q9R254;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE CD40 LIGAND. 16, last annotation update)
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE DAWLEY;
RA Hallett K.M., Oaks M.K.;
RT "Nucleotide Sequence of the Rat CD40 ligand."
RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF16582; AAD2460.1;
DR HSSP; P27548; ICDA.
DR InterPro: IPR000478;
DR Pfam: PF00229; TNF_1;
DR ProDom: PD008600; TNF_1;
DR PROSITE; PS00251; TNF_1;
DR PROSITE; PS00499; TNF_2;
DR SMART; SM00207; TNF_1;
SQ SEQUENCE 260 AA; 29259 MW; B3D3757DEB0DB73A CRC64;

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Query Match: 33.3%; Score 827; DB 11; Length 260;
Best Local Similarity 64.8%; Pred. No. 7.7e-57;
Matches 171; Conservative 28; Mismatches 53; Indels 12; Gaps 4;
QY 209 PGDRCIKESGLPDSALRQOMELKGLQRL-EVAFSHYQKALFPDGHRRDLKEDER 267
DB 8 PPSRSV--ATGLPASKMIFVLLTFLITOMIGSVLFAVYL-----HRLDVEEBA 57
QY 268 NLHEDFVEMKTIORCNGERSLNLNCEIKSQPEGVKDIMLNKEETKENSEFEMOKG 327
DB 58 SLHEDFVFKKLRCKNGEGSLNLNCEIKSQPEGVKDIMLNKEETKENSEFEMOKG 116
QY 328 QNPQIAHVISSASKTTSVLOAENGKYTWSNNLVTLNKGKQLTVRKGLIYIYAQVF 387
DB 117 EDPQIAHVISSASKTTSVLOAENGKYTWSNNLVTLNKGKQLTVRKGLIYIYAQVF 176
QY 388 CSNREASSOAPFLASLCLKSPGRRERILLRANTHSSAKPCGQOSIHGVEFLQPCASV 447
DB 177 CSNREPLSORPFLVSLMLKSSGSEERILLRANTHSSSKLCEQOSIHGVEFLQPCASV 236
QY 448 FNVVTDPSOVSHGTGFTSFGLTKL 471
DB 237 FNVVTEASQVHIGIGFSISGLTKL 260

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RESULT 4
Q97748 PRELIMINARY; PRT: 335 AA.
AC Q97748;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DE CD40 LIGAND. 16, last annotation update)
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

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OC Bovidae; Bovinae; Bos.
OX NCBI_TaxId=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=93213261; PubMed=8460993;
RA Suzuki Y., Yin Y., Makino M., Kurimura T., Wakamiya N.;
RT "Cloning and sequencing of a cDNA coding for bovine conglutinin.";
RL Biochem. Biophys. Res. Commun. 191:335-342(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=93277452; PubMed=7684896;
RA Lu J., Laursen S., Thiel S., Jensenius J., Reid K.;
RT "The cDNA cloning of conglutinin and identification of liver as a
RL Biochem. J. 292:157-162(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=94128104; PubMed=8297370;
RA Kawasaki N., Itoh N., Kawasaki T.;
RT "Gene organization and 5'-flanking region sequence of conglutinin: a
RL Biochem. Biophys. Res. Commun. 198:597-604(1994).
DR EMBL; D25302; BAA04983.1; -.
DR EMBL; D25286; BAA04983.1; JOINED.
DR EMBL; D25287; BAA04983.1; JOINED.
DR EMBL; D25289; BAA04983.1; JOINED.
DR EMBL; D25300; BAA04983.1; JOINED.
DR EMBL; D25301; BAA04983.1; JOINED.
DR HSSP; P35247; 1B08.
DR InterPro; IPR000087; -.
DR InterPro; IPR001304; -.
DR Pfam; PF00059; Lectin_C; 1.
DR Pfam; PF00059; Collagen; 2.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_2; 1.
DR SMART; SM00034; CLECT; 1.
DR CONFLICT 236 E -> V (IN REF. 2).
SO SEQUENCE 335 AA; 34702 MW; 39D3A30BC76C134C CRC64;

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[illegible]

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Db      275 DIST 278

RESULT      5
ID         077087 PRELIMINARY; PRT; 890 AA.
AC         077087
DT      01-NOV-1998 (TREMBLrel. 08, Created)
DT      01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT      01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE      FIBRILLIN COLLAGEN CHAIN FAP1 ALPHA.
OS      Alvinella pompejana.
OC      Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canallipalpata;
CC      Terebellida; Alvineillidae; Alvinella.
CX      NCBI_TaxId=6376;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Sloc F.-X., Gall F., Exposito J.-Y., Garrone R., Deutsch J.:
RL      Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
DR      EMBL; AF053538; AAC35289.2; -.
DR      InterPro: IPR000087; -.
DR      InterPro: IPR000885; -.
DR      Pfam: PF01391; Collagen; 10.
DR      Pfam: PF01410; COLFI; 1.
DR      ProDom: PD002078; ?; 1.
DR      SMART: SM00038; COLFI; 1.
KW      Collagen.
SQ      SEQUENCE      890 AA; 88136 MW; 5ZC0756FA70CA90C CRC64;

Query Match          20.1%; Score 499.5; DB 5; Length 890;
Best Local Similarity 47.5%; Pred. No. 1,1e-30;
Matches 115; Conservative 11; Mismatches 73; Indels 43; Gaps

OY      14 PLGNLC-----AEKSLSORVPNTCTLYWCSP--TENGLPGRDGRGREGPSEKG 63
       | ||| | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB      320 PAGNTPGPGRPGRGAGIGL--RGERG-----KGRAGDPPTGPTGPHMDGTGERGEDG 376
       ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |

OY      64 DPGLPGPMGLSGLO-----GPTGVGPKGENSAGEP---GPRGERLSG 105
       ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |
DB      371 PGCLPGPTGPGRPGGERGFVGLPGERGERPGPGAPGRPEGPAGPBGDTGPRGERGSPG 430
       ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |

OY      106 PELPLPGIPGAGKEGEPGKCNICPOGRP---GPRGEAGPKGEVCAPMGOGSTGAKGSTG 167
       | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      431 PSGAPGAPGAAGEGPEGKDGLLPLACGRPCDKGPPCPGPGIACGAMQGLRGPPGPTG 490
       | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY      163 PKGERAPGVQGAPAGNMGAAGPAPPA---GPGAGCSRRPPLGKGRRGVCDGNGEGSG 219
       | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      491 PGGERERGERGAPGVGPGPPAGAPGGOGSKGERCAAPKGDKGMPPMELDSMOG 550
       | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY      220 LP 221
       |
DB      551 TP 552

RESULT      6
ID         090796 PRELIMINARY; PRT; 888 AA.
AC         090796
DT      01-NOV-1996 (TREMBLrel. 01, Created)
DT      01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT      01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE      ALPHA-1 TYPE XI COLLAGEN (FRAGMENT).
OS      Gallus gallus (Chicken).
CC      Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
CX      NCBI_TaxId=9031;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      STRAIN-WHITE LEGHORN; TISSUE-Limb;
RL      MEDLINE=93054557; PubMed=1429607;
RX      Nah H.D., Barembaum M., Upholt W.B.;
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Query Match          20.1%  Score 499.5;  Db 5;  Length 890;
Best Local Similarity 47.5%  Pred. No. 1,1e-30;
Matches 115;  Conservative 11;  Mismatches 73;  Indels 43;  Gaps 8;

OY  14  PLGNLGG-----AEMKSLSORSVPTCTLMWCSPP---TENGJLPGRDGRDREGPRGEGK 63
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB  320  PAGNTGPPRPPGPGAGIGKL--RGERG-----KPRAGDPRGTFRTGMDTKKERGEDG 370
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY  64  DPLGPGPMGLSLGLQ-----GPTGVPVPGKGENSGAGEP---GPKGERGLSG 105
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB  371  PPELPGTGTGPPGQGERGTFVGLPGERGERGPPGAPGRGEPGAPGEPGDTGPRGERGSPG 430
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY  106  PPELPGTGTGPPGQGERGTFVGLPGERGERGPPGAPGRGEPGAPGEPGDTGPRGERGSPG 162
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB  431  PSCAPGAPGAAGPGRPGKDLPLGLAGRPDKGPPCPPPGGLAGAPMGGLRGPPTG 490
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY  163  PKBERCAPGVQGAAGNMGACAPAGA---GPGCAPSRRPPGLKGDGNGVGDRIKESG 219
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB  491  PGERGERGERGAPGVGRPVGPPGPAGAPGQOGSKGERGAAGKGRDKGWPGMPLQGMQG 550
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY  220  LP 221
DB  551  TP 552

RESULT 6
ID 090796 PRELIMINARY; PRT: 888 AA.
AC 090796;
DT 01-NOV-1996 (TREMBLREL. 01, Created)
DT 01-NOV-1996 (TREMBLREL. 01, Last sequence update)
DE 01-MAR-2001 (TREMBLREL. 16, Last annotation update)
DE ALPHA-1 TYPE XI COLLAGEN (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
OX 111
RP SEQUENCE FROM N.A.
RC STRAIN=WHITE LEGHORN; TISSUE=LIMB;
RA MEDLINE=93054557; PubMed=1429607;
RX Nah H.D., Barembaum M., Upholt W.B.;

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... and courtin' some cause Marshall

RESULT 13
Q9U1T5

Matches	100; Conservative	18; Mismatches	60; Indels	42; Gaps	4;
Oy	41	PRENGLPR--DGRDREGPRGKGDPLGPMGLSLGQPTG-----	82		
Db	1314	PGDPGPPGELGPAAGDGVGDKEDGDPGPGPPSGGAPPGPGKRGPGAGAGR	1373		
Oy	83	-----VCPKGENSGAGEPGPKGKGLSGPPGLPGIPGPKGEGPSGK	124		
Db	1374	QSEKAGKGEAGGAGGPGKTPGVGPGGPKGPGEGLRGIPGPGEGGLPAAAGDGP	1433		
Oy	125	QGNIGQGAKGPPGGEAPKGVGAPMGSGTCAKSGTSGKGEAGAGVGCAP---	GNAGA 181		
Db	1434	---MGPPGLGLGDPKSGKGGHPGLGLGPPGEGKGRGLGTGSPGAKGGGI	1490		
Oy	182	AGPAGPAGPGAGPSRGGPGLGDRGVGDRGKESGIP	221		
Db	1491	PGPAGPPGPPGPPGLGPPGPKGKSGTGPAQKDGSLP	1530		
RESULT 14					
ID	0901T6	PRELIMINARY;	PRT;	1818	AA.
AC	0901T6;				
DT	01-MAY-2000 (TREMblrel. 13, Created)				
DT	01-MAY-2000 (TREMblrel. 13, Last sequence update)				
DT	01-MAR-2001 (TREMblrel. 16, Last annotation update)				
DE	COLLAGEN TYPE XI ALPHA-A ISOFORM B.				
GN	COL1A1.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=20455728; PubMed=10486316;				
RA	Annunen S., Korkko J., Czarny M., Warman M.L., Brunner H.G.,				
RA	Kaartainen H., Mulliken J.B., Tremblay L., Brooks D.G., Cox G.F.,				
RA	Crusberg J.R., Curtis M.A., Davenport S.L.H., Friedrich C.A.,				
RA	Kallia I., Krawczynski M.R., Jancos-Bielenska A., Mukai S.,				
RA	Allen B.R., Shimo N., Sommer M., Vilkula M., Zlotogora J.,				
RA	Prockop D.J., Ala-Kokko L.;				
RT	*Splicing Mutations of 54 bp Exons in the COL1A1 Gene Cause Marshall				
RT	Syndrome but Other Mutations Cause Overlapping Marshall/Stickler				
RT	Phenotypes.";				
RL	Am. J. Hum. Genet. 65:974-983(1999).				
DR	EMBL; AF101112; AAF04726.1; -				
DR	EMBL; AF101079; AAF04726.1; JOINED.				
DR	EMBL; AF101080; AAF04726.1; JOINED.				
DR	EMBL; AF101081; AAF04726.1; JOINED.				
DR	EMBL; AF101082; AAF04726.1; JOINED.				
DR	EMBL; AF101083; AAF04726.1; JOINED.				
DR	EMBL; AF101084; AAF04726.1; JOINED.				
DR	EMBL; AF101085; AAF04726.1; JOINED.				
DR	EMBL; AF101086; AAF04726.1; JOINED.				
DR	EMBL; AF101087; AAF04726.1; JOINED.				
DR	EMBL; AF101088; AAF04726.1; JOINED.				
DR	EMBL; AF101089; AAF04726.1; JOINED.				
DR	EMBL; AF101090; AAF04726.1; JOINED.				
DR	EMBL; AF101091; AAF04726.1; JOINED.				
DR	EMBL; AF101092; AAF04726.1; JOINED.				
DR	EMBL; AF101093; AAF04726.1; JOINED.				
DR	EMBL; AF101094; AAF04726.1; JOINED.				
DR	EMBL; AF101095; AAF04726.1; JOINED.				
DR	EMBL; AF101096; AAF04726.1; JOINED.				
DR	EMBL; AF101097; AAF04726.1; JOINED.				
DR	EMBL; AF101098; AAF04726.1; JOINED.				
DR	EMBL; AF101099; AAF04726.1; JOINED.				
DR	EMBL; AF101100; AAF04726.1; JOINED.				
DR	EMBL; AF101101; AAF04726.1; JOINED.				
DR	EMBL; AF101102; AAF04726.1; JOINED.				
DR	EMBL; AF101103; AAF04726.1; JOINED.				
DR	EMBL; AF101104; AAF04726.1; JOINED.				
DR	EMBL; AF101105; AAF04726.1; JOINED.				

